



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96045

TO: Mark Navarro
Location: 8A15
Art Unit: 1645
Friday, June 06, 2003

Case Serial Number: 09/150947

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291 *BOB*

barbara.obryen@uspto.gov

Search Notes

Mark,
all of the requested seqs contain bunches of Xaa's. With standard search parameters, Xaa's in either the query seq or the database seq are considered non-matches, so I don't know how useful you will find these results to be. We have an alternative search that can be done in cases like this, called "DX matching table". With this matching table, Xaa in the query sequence matches anything in the database seq. Xaa in a database seq still is considered a non-match.
If you think DX matching table results would be more useful to you, please let me know.
Barb

O'Bryen, Barbara

From:
Sent:
To:
Subject:

Navarro, Albert
Thursday, June 05, 2003 1:38 PM
O'Bryen, Barbara
09/150,947

Mark Navarro
1645
306-3225
8A15

Hello Barb,

Could I trouble you for a search and an interference search of:

SEQ ID NO: 13-18

Thanks

Mark



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:47:43 ; Search time 33.9394 Seconds

(without alignments)
39.261 Million cell updates/sec

Title: US-09-150-947f-13

Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

A.Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	77.4	233	21	AAV93741	Amino acid sequence
2	24	77.4	258	23	ABP29565	Streptococcus poly
3	23	74.2	17	23	ABP76254	Staphylococcus aur
4	23	74.2	24	21	AAV97855	Staphylococcus aur
5	23	74.2	24	22	AAV72193	Peptide from regio
6	23	74.2	29	22	AAV59147	Human brain expro
7	23	74.2	29	22	AAV71683	Human bone marrow
8	23	74.2	29	22	AAV31976	Peptide #6013 enco
9	23	74.2	29	23	ABG41496	Human peptide enco
10	23	74.2	228	22	AAV63856	Amino acid sequence

11	23	74.2	238	12	AAV13208	Staphylococcal ent
12	23	74.2	238	14	AAV45016	Staphylococcal ent
13	23	74.2	238	22	AAV67343	Staphylococcus aur
14	23	74.2	238	23	ABP76239	Staphylococcus aur
15	23	74.2	239	12	AAV13207	Staphylococcal ent
16	23	74.2	239	14	AAV45015	Staphylococcal ent
17	23	74.2	239	20	AAV08254	Staphylococcal gro
18	23	74.2	239	20	AAV08255	Staphylococcal gro
19	23	74.2	239	20	AAV08256	Staphylococcal gro
20	23	74.2	239	20	AAV08257	Staphylococcal gro
21	23	74.2	239	20	AAV08258	Staphylococcal gro
22	23	74.2	239	20	AAV08251	Staphylococcal gro
23	23	74.2	239	20	AAV08252	Staphylococcal gro
24	23	74.2	239	20	AAV08253	Staphylococcal gro
25	23	74.2	239	22	AAV67342	Staphylococcus aur
26	23	74.2	239	23	ABP76238	Staphylococcus aur
27	23	74.2	266	21	AAV70108	Staphylococcal ent
28	23	74.2	266	23	ABP79507	Staphylococcal ent
29	23	74.2	311	22	ABG17229	Novel human diagno
30	23	74.2	405	21	AAV26155	B. cereus zwitterm
31	22	71.0	10	19	AAV64639	Synthetic SSB pept
32	22	71.0	10	19	AAV64638	Synthetic SSB pept
33	22	71.0	12	19	AAV64636	Synthetic SSB pept
34	22	71.0	12	19	AAV64637	Synthetic SSB pept
35	22	71.0	13	19	AAV64640	Synthetic SSB pept
36	22	71.0	13	19	AAV64641	Synthetic SSB pept
37	22	71.0	13	19	AAV64646	Synthetic SSB pept
38	22	71.0	14	19	AAV64644	Synthetic SSB pept
39	22	71.0	14	19	AAV64645	Synthetic SSB pept
40	22	71.0	17	23	ABP76253	Staphylococcus aur
41	22	71.0	17	23	ABP76257	Streptococcus pyog
42	22	71.0	17	23	ABP76258	Enterotoxin, pyoge
43	22	71.0	24	19	AAV64642	Synthetic SSB pept
44	22	71.0	24	21	AAV97854	Staphylococcus aur
45	22	71.0	24	21	AAV97859	Group A streptococ

ALIGNMENTS

RESULT 1
ID AAV93741 standard; Protein: 233 AA.
AC AAV93741;
XX 03-OCT-2000 (first entry)
XX
XX Amino acid sequence of the mature SMEZ-2 superantigen protein.
DE
XX Sperantigen; SMEZ-2; SPE-G; SPE-H; SPE-J; Streptococcal disease;
XX Kwasaki syndrome; T cell activation; cancer therapy.
KM
XX Streptococcus pyogenes.
OS
XX WO200039159-A1.
PN
XX 06-JUL-2000.
PD
XX 24-DEC-1999; 99WO-N00228.
PE
XX 24-DEC-1998; 98NZ-0333589.
PR
XX (AUCK-) AUCKLAND UNISERVICES LTD.
PA
XX Fraser JD, Proft T;
XX WPI, 2000-452370/39.
XX N-PSDB; AAA47147.
XX Novel superantigens from streptococcus pyogenes useful for genotyping
XX streptococcus pyogenes clones expressing SMEZ-2 and for diagnosing a
XX Kawasaki syndrome

XX PS Claim 2; Fig 2; 72pp; English.

CC The present sequence represents the SMEZ-2 superantigen protein. The

CC specification describes superantigen proteins SMEZ-2, SPE-G, SPE-H

CC and SPE-I. The superantigen polynucleotides and polypeptides are

CC used for subtyping Streptococci. They are also used for diagnosing

CC Streptococcal disease. The superantigens are used in diagnosis of

CC disease such as Kawasaki syndrome. They are also useful to recruit

CC and activate T cells in a relatively non-specific fashion since

CC they bind a large number of T cell receptor molecules by binding to the

CC Vbeta domain. Superantigen constructs are useful in cancer therapy.

XX SQ Sequence 233 AA;

Query Match 77.4%; Score 24; DB 21; Length 233;

Best Local Similarity 50.0%; Pred. No. 73;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10

DB 149 KTTVTAQED 158

RESULT 2

ABP29565

ID ABP29565 standard; Protein; 258 AA.

XX AC ABP29565;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 8306.

XX KM Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;

XX KM group A streptococcus; Streptococcus pyogenes; antibacterial;

XX KM antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus pyogenes.

XX PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX PI Tettelin H;

XX DR WPI: 2002-352536/38.

XX DR N-PSDB; ABN70196.

XX PT New Streptococcus protein for the treatment or prevention of infection

XX PT or disease caused by Streptococcus bacteria, such as meningitis, and

XX PT for detecting a compound that binds to the protein -

XX PS Claim 1; Page 3947; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

XX SQ Sequence 258 AA;

Query Match 77.4%; Score 24; DB 23; Length 258;

Best Local Similarity 50.0%; Pred. No. 81;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10

DB 174 KTTVTAQED 183

RESULT 3

ABB76254

ID ABB76254 standard; Peptide; 17 AA.

XX AC ABB76254;

XX DT 09-AUG-2002 (first entry).

XX DE Staphylococcus aureus enterotoxin C1 peptide fragment.

XX KM Enterotoxin C; SECI; superantigen; antigen; tumour; cancer;

XX KM antitumour; therapy.

XX OS Staphylococcus aureus.

XX PN US2002051765-A1.

XX PD 02-MAY-2002.

XX PF 19-DEC-2000; 2000US-0741503.

XX PR 31-JAN-1994; 94US-0189424.

XX PR 19-JUN-1995; 95US-0491746.

XX PR 03-OCT-1989; 89US-0416530.

XX PR 17-JAN-1990; 90US-0465577.

XX PR 17-JAN-1991; 91WO-US00342.

XX PR 01-JUN-1992; 92US-0891718.

XX PR 02-MAR-1993; 93US-0025144.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR WPI: 2002-415198/44.

XX PT Reagent for treating cancer without the need for e.g. radiotherapy,

XX PT comprises a specific V beta subset of T cells sensitized to a growing

XX PT tumor and stimulated with superantigens -

XX PS Disclosure; Page 4; 17pp; English.

CC The present sequence corresponds to amino acids 151-167 of

CC enterotoxin C1 (SECI, see ABB76238) of Staphylococcus aureus.

CC Sequence similarities are found in the corresponding regions

CC of other staphylococcal enterotoxins and streptococcal pyrogenic

CC exotoxins (see ABB76252-59). In the present invention, synthetic

CC polypeptides useful in tumour therapy and in blocking or destroying

CC autoreactive T and B lymphocyte populations are characterised by

CC substantial structural homology to staphylococcal enterotoxin A and

CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with

CC statistically significant sequence homology and similarity,

CC including alignment of cysteine residues and similar hydrophaty

CC profiles. These superantigens are used to treat solid tumours,
CC including their metastases, without radiation, surgery or standard
CC chemotherapeutic agents. A claimed method of human cancer treatment
CC involves contacting haematopoietic cells from a patient with one or
CC more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells
CC into the patient to induce an in vivo therapeutic, tumouricidal
CC reaction.

XX Sequence 17 AA:

SO Query Match 74.2%; Score 23; DB 23; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.8;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXKXTXQEXD 10
| | | |
Db 1 KRVTVADEL D 10

RESULT 4
ID AA97855 standard; peptide: 24 AA.
AA97855
AC AA97855;
DT 29-AUG-2000 (first entry)
DE Staphylococcus aureus enterotoxin SEC, conserved region 2.
XX Staphylococcal infection; enterotoxin; septic shock; toxic shock;
KW vaccine; antibody.
XX Staphylococcus aureus.
OS
PN WO200020598-AI.
PD 13-APR-2000.
PF 24-SEP-1999; 99WO-US22180.
PR 07-OCT-1998; 98US-0168303.
PR 18-JUN-1999; 99US-0335581.
XX (UYNQ) UNITV ROCKEFELLER.
PA Bannan JD, Visvanathan K, Zabriskie JB:
PI MPI: 2000-303782/26.
XX
XX The invention relates to novel peptides (AA97838-Y97843) comprising a
CC consensus amino acid sequence derived from two conserved regions
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N
CC (AA97863) and consensus region 2a (a preferred consensus region 2) has
CC the sequence R-X6-X7-X8-
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
CC (AA97864), where: X1, X6, X13 and X24 are each independently selected
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
CC the group consisting of any amino acid;
CC X3, X5 and X26 are each independently selected from the group consisting
CC of any amino acid and of no amino acid;
CC X27 is either L or Y.
CC The invention also relates to serum antibodies induced by the peptides
CC which provide protection against, or reduce the severity of toxic shock

CC	and septic shock caused by the staphylococcal and streptococcal
CC	pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
CC	the enterotoxins of staphylococcus aureus (which are also pyrogenic
CC	exotoxins) constitute a family of structurally related toxins which
CC	share similar biological activities. They stimulate CD4+, CD8+ and
CC	gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
CC	elements on the lateral face of the T-cell receptor (TCR) while
CC	simultaneously binding the lateral face of the class II major
CC	histocompatibility complex (MHC) of antigen presenting cells. This causes
CC	aberrant proliferation of T-cells, which stimulates other components of
CC	the immune system, causing injury to the host. The peptides are used to
CC	prevent, treat or protect against toxic shock and septic shock resulting
CC	from bacterial infections in mammals, particularly humans. The peptides
CC	are used for inducing serum antibodies that bind at least one
CC	staphylococcal enterotoxin or streptococcal exotoxin and both the
CC	peptides and antibodies can be used in diagnostic assays to aid in the
CC	diagnosis of disease related to the presence of bacterial toxins. Nucleic
CC	acids encoding a peptide of the invention can be used for the production
CC	of the peptides for diagnostic reagents, as vaccines and for therapies
CC	for pyrogenic exotoxin related diseases. Vectors expressing high levels
CC	of the peptides can be used in immunotherapy and immunoprophylaxis when
CC	expressed in humans. The antibodies are used for passive immunisation
CC	therapy to prevent or increase resistance to toxic shock syndrome or
CC	septic shock and to ameliorate the effects of conditions associated with
CC	the presence of staphylococcal or streptococcal pyrogenic toxins. The
CC	amino acid sequences of the peptides are sufficiently common that they
CC	can be used for eliciting antibodies which are cross-reactive with toxins
CC	derived from various bacteria. Sequences AAY7853-Y97861 represent
CC	conserved region 2 of various staphylococcus aureus enterotoxins and
CC	Group A streptococcal pyrogenic exotoxins.
XX	Sequence 24 AA:
XX	5Q
XX	Query Match 74.2% Score 23; DB 21; Length 24;
XX	Best Local Similarity 50.0%; Pred. No. 14;
XX	Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	1 KXXXTXQEXD 10
DB	1 KKSVTAGELD 10
XX	1 1 1 1 1
XX	RESULT 5
XX	AAV72193
ID	AAV72193 standard; peptide: 24 AA.
XX	XX
XX	AAV72193;
XX	XX
XX	24-APR-2001 (first entry)
XX	XX
DE	Peptide from region 2 of staphylococcal enterotoxin SEC.
XX	XX
KW	Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
KM	staphylococcal enterotoxin; human immunodeficiency virus; T cell;
KW	autoimmune disease; immunisation.
XX	XX
OS	Staphylococcus sp.
XX	XX
PN	WO200078790-A2.
XX	XX
PD	28-DEC-2000.
XX	XX
PF	16-JUN-2000; 2000WO-US16680.
XX	XX
PR	18-JUN-1999; 99US-0336627.
XX	XX
XX	(UYRQ) UNIV ROCKEFELLER.
PA	XX
PI	Vasvanathan K, Zabriskie JB;
XX	XX
DR	WPI; 2001-080820/09.
XX	XX
PT	Providing protection against, and reducing the severity of, human

PT Immunodeficiency virus infections and associated deleterious effects,
PT using peptides from homologous sequences of staphylococcal and
XX streptococcal toxins
PS Disclosure; Page 36; 76pp; English.
XX
CC The present sequence is a peptide from region 2 of staphylococcal
CC enterotoxin SEC.
CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
CC against the peptide are useful for inhibiting biogenesis of
CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency
CC virus (HIV), inhibiting HIV replication and protecting a mammal against
CC the deleterious effects of HIV. The peptide is also used to ameliorate
CC the effects of autoimmune diseases associated with the presence of HIV.
CC The Ab is used for passively immunizing a mammal against the deleterious
CC effects of HIV.
XX
SQ Sequence 24 AA;
Query Match 74.2%; Score 23; DB 22; Length 24;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 KXXXTXQEXD 10
DB 1 KKSVTQAEID 10
RESULT 6
ID AAM59147 standard; Protein; 29 AA.
XX AAM59147;
XX
XX 05-NOV-2001 (first entry)
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31252.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer.
OS Homo sapiens.
XX
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00667.
PE
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI: 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX Example 4; SEQ ID NO: 31252; 650pp + Sequence Listing; English.
PS
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 29 AA;
Query Match 74.2%; Score 23; DB 22; Length 29;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 KXXXTXQEXD 10
DB 10 KALSTGQEID 19
RESULT 7
ID AAM71683 standard; Protein; 29 AA.
XX AAM71683;
XX
XX 06-NOV-2001 (first entry)
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31989.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00668.
PE
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI: 2001-488900/53.
DR
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 31989; 650pp + Sequence Listing; English.
PS
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
XX
SQ Sequence 29 AA;
Query Match 74.2%; Score 23; DB 22; Length 29;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 KXXXTXQEXD 10
DB 10 KALSTGQEID 19

RESULT 8
 AAM31976
 ID AAM31976 standard; Protein: 29 AA.
 AC AAM31976;
 XX
 XX
 XX 17-OCT-2001 (first entry)
 DE Peptide #6013 encoded by probe for measuring placental gene expression.
 XX
 XX Probe: microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200157272-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00663.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PT WPI; 2001-488897/53.
 DR
 XX WPI; 2001-488897/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 XX Claim 27; SEQ ID NO 32245; 654bp; English.
 PS
 XX The present invention relates to single exon nucleic acid probes (SENP;
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 XX Sequence 29 AA:
 SO
 Query Match 74.2%; Score 23; DB 22; Length 29;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXKXQEND 10
 Db 10 KALSTQGEID 19
 RESULT 9
 ABG41496
 ID ABG41496 standard; Peptide: 29 AA.
 AC ABG41496;
 XX
 XX 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 31161.
 XX
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KM chronic obstructive pulmonary disease; interstitial lung disease;
 KM familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KM tuberos sclerosis; Gaucher's disease; Niemann-Pick disease;
 KM Hernanaky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KM pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KM primary ciliary dyskinesia; pulmonary hypertension;
 XX hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200186003-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00665.
 PF
 XX 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PT WPI; 2002-114183/15.
 DR
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 PT
 XX Claim 27; SEQ ID NO 31161; 654bp; English.
 PS
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12614 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarray having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberos sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hernanaky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 29 AA;
 Query Match 74.2%; Score 23; DB 23; Length 29;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXOEXD 10
 DB 10 KALSTGOEID 19
 RESULT 10
 AAG63856
 ID AAG63856 standard; Protein: 228 AA.
 AC AAG63856;
 XX
 DT 29-OCT-2001 (first entry)
 DE Amino acid sequence of a modified Staphylococcal enterotoxin C1.
 KW Enterotoxin C1; SEC-SER; Infectious disease; mastitis.
 OS Synthetic.
 OS Staphylococcus sp.
 XX
 PN WO200160851-A1.
 PD 23-AUG-2001.
 PF 31-OCT-2000; 2000WO-KR01241.
 PR 17-FEB-2000; 2000KR-0007612.
 PA (GLDS) LG CHEM LTD.
 PI Lee H, Park Y, Han K, Chang B, Lee Y;
 DR WPI: 2001-522585/57.
 DR N-PSDB: AAH74983.
 PT Producing stable modified Staphylococcal toxin polypeptide for treating
 PT infectious diseases, e.g. mastitis, in animals, involves substituting
 PT cysteine at specified position of modified Staphylococcal toxin C1 with
 PT serine.
 PS Claim 1; Page 59-60; 64pp; English.
 CC The present sequence represents a modified Staphylococcal enterotoxin C1,
 CC designated SEC-SER. The modified toxin is characterised in that the
 CC 95th amino acid (cysteine) is substituted with serine. This results in
 CC a toxin that has improved stability. The modified enterotoxin is
 CC useful for preventing or treating infectious diseases due to
 CC microorganisms in animals such as cows, pigs, horses, sheep, hens,
 CC dogs and cats, e.g. mastitis in cows.
 XX
 SQ Sequence 228 AA;
 Query Match 74.2%; Score 23; DB 22; Length 228;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXOEXD 10
 DB 140 KRSVTAOEID 149
 RESULT 11
 AAR13208
 ID AAR13208 standard; Protein: 238 AA.
 AC AAR13208;
 XX

DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin C3.
 KW SEC3; cancer treatment; pyrogen; tumouricide.
 OS Staphylococcus aureus.
 PN WO9110680-A.
 PD 25-JUL-1991.
 PF 17-JAN-1991; 91WO-US00342.
 PR 17-JAN-1990; 90US-0466577.
 PA (TERM/) TERMAN D S;
 PI Terman DS;
 DR WPI: 1991-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure; Fig 1; 74pp; English.
 CC SEC3 was isolated and purified from S.aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of cysteine residues and
 CC similar hydrophathy profiles.
 XX See AAR13203-R13211.
 SQ Sequence 238 AA;
 Query Match 74.2%; Score 23; DB 12; Length 238;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXOEXD 10
 DB 150 KRSVTAOEID 159
 RESULT 12
 AAR45016
 ID AAR45016 standard; Protein: 238 AA.
 AC AAR45016;
 XX
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SEC3.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 OS Staphylococcus aureus.
 PN WO9324136-A.
 PD 09-DEC-1993.
 PF 01-JUN-1993; 93WO-US05213.
 PR 01-JUN-1992; 92US-0891718.
 XX

PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 XX Stone JL, Terman DS;
 PI WPI: 1993-405418/50.
 XX
 DR WPI: 1993-405418/50.
 XX
 XX Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 XX
 XX Disclosure: Fig 1; 90pp; English.
 XX
 CC The sequences given in AAK45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumoricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumoricidal activity and toxicity identical to that
 CC observed for the Protein A pertussis system. They may be administered
 CC by i.v. injection.
 CC
 SQ Sequence 238 AA:
 Query Match 74.2%; Score 23; DB 14; Length 238;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 KXXXTXQEXD 10
 DB 150 KKSVTAAQELD 159
 RESULT 13
 AAB67343
 ID AAB67343 standard; peptide; 238 AA.
 XX AAB67343;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin C3 protein.
 XX
 KW Tumour; cancer; immune; enterotoxin.
 XX
 OS Staphylococcus aureus.
 XX
 PN US6180097-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 30-OCT-1998; 98US-0183437.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) TERMAN D S.
 PA
 PI Terman DS;
 PI
 XX WPI: 2001-158657/16.
 DR
 XX
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro
 PT or in vivo comprises exogenous nucleic acids encoding a superantigen
 PT and a costimulatory molecule -
 XX
 XX Disclosure: Fig 2; 16pp; English.
 PS
 XX The present invention relates to a tumour cell capable of stimulating

CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule
 CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 CC
 SQ Sequence 238 AA:
 Query Match 74.2%; Score 23; DB 22; Length 238;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 KXXXTXQEXD 10
 DB 150 KKSVTAAQELD 159
 RESULT 14
 ABB76239
 ID ABB76239 standard; Protein; 238 AA.
 XX ABB76239;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin C3.
 XX
 KW Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
 KW antitumour; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 208 /note="given as 'O' in the specification"
 FT
 PN US2002051765-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 19-DEC-2000; 2000US-0741503.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) TERMAN D S.
 PA
 PI Terman DS;
 PI
 XX WPI: 2002-415198/44.
 DR
 XX
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens -
 XX
 XX Disclosure: Fig 2; 17pp; English.
 PS
 XX The present sequence is the protein sequence of enterotoxin C3
 CC (SEC3) of Staphylococcus aureus. Similarity is shown, in several
 CC stretches of sequence, between staphylococcal enterotoxins,
 CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative
 CC toxins (see ABB76234-44). In the present invention, synthetic
 CC polypeptides useful in tumour therapy and in blocking or destroying
 CC autoreactive T and B lymphocyte populations are characterised by
 CC substantial structural homology to staphylococcal enterotoxin A and
 CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with

statistically significant sequence homology and similarity (Z value of Lipman and Pearson algorithm in Monte Carlo analysis exceeding 6) to include alignment of cysteine residues and similar hydrophathy profiles. These superantigens are used to treat solid tumors, including their metastases, without radiation, surgery or standard chemotherapeutic agents. A claimed method of human cancer treatment involves contacting haematopoietic cells from a patient with one or more superantigens ex vivo to generate stimulated cells, selecting a specific V beta subset of cells, and reintroducing these cells into the patient to induce an in vivo therapeutic, tumoricidal reaction.

Sequence 238 AA;

Query Match 74.2%; Score 23; DB 23; Length 238;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
| | | |
DB 150 KSVTAQELD 159

RESULT 15

AAR13207 AAR13207 standard; Protein; 239 AA.

AC AAR13207;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin C1.

KW SEC1; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.

FN W09110680-A.

PD 25-JUL-1991.

PF 17-JAN-1991; 91MO-US00342.

PR 17-JAN-1990; 90US-046577.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI: 1991-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -
administered by IV injection, having same tumoricidal activity
as Staphylococcal protein A without potential toxic reactions

PS Disclosure: Fig 1; 74pp; English.

SEC1 was isolated and purified from S.aureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with lipoprotein to attenuate toxic reaction to SEC1. Synthetic polypeptides having structural homology to staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydrophathy profiles.
See AAR13203-R13211.

SO Sequence 239 AA;

Query Match 74.2%; Score 23; DB 12; Length 239;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
| | | |
DB 151 KSVTAQELD 160

Search completed: June 5, 2003, 16:00:22
Job time : 34.9394 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:23:33 ; Search time 8.78788 Seconds
(without alignments)
33.481 Million cell updates/sec

Title: US-09-150-947F-13

Perfect score: 31

Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Dackfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	74.2	17	4	US-08-896-933-6
2	23	74.2	17	4	US-09-314-235-6
3	23	74.2	24	3	US-08-838-413A-20
4	23	74.2	238	4	US-08-896-933-28
5	23	74.2	238	4	US-09-314-235-28
6	23	74.2	239	4	US-08-896-933-27
7	23	74.2	239	4	US-09-314-235-27
8	23	74.2	266	4	US-09-144-776B-14
9	22	71.0	17	4	US-08-896-933-4
10	22	71.0	17	4	US-08-896-933-12
11	22	71.0	17	4	US-08-896-933-14
12	22	71.0	17	4	US-08-896-933-15
13	22	71.0	17	4	US-08-896-933-16
14	22	71.0	17	4	US-08-896-933-17
15	22	71.0	17	4	US-09-314-235-4
16	22	71.0	17	4	US-09-314-235-12
17	22	71.0	17	4	US-09-314-235-14
18	22	71.0	17	4	US-09-314-235-15
19	22	71.0	17	4	US-09-314-235-16
20	22	71.0	17	4	US-09-314-235-17
21	22	71.0	24	3	US-08-838-413A-19
22	22	71.0	24	3	US-08-838-413A-24
23	22	71.0	191	4	US-08-858-207A-381
24	22	71.0	221	4	US-08-896-933-29
25	22	71.0	221	4	US-09-314-235-29
26	22	71.0	239	4	US-08-896-933-26
27	22	71.0	239	4	US-09-314-235-26

28	22	71.0	239	4	US-09-144-776B-10	Sequence 10, Appl
29	22	71.0	251	4	US-09-144-776B-16	Sequence 16, Appl
30	22	71.0	255	1	US-08-446-918A-2	Sequence 2, Appl
31	22	71.0	255	2	US-08-580-806-2	Sequence 2, Appl
32	22	71.0	266	4	US-09-414-276-8	Sequence 8, Appl
33	22	71.0	266	4	US-09-144-776B-6	Sequence 6, Appl
34	22	71.0	266	4	US-09-190-824-2	Sequence 8, Appl
35	22	71.0	292	4	US-09-144-776B-8	Sequence 2, Appl
36	22	71.0	922	2	US-08-464-402-2	Sequence 2, Appl
37	22	71.0	922	4	US-09-054-775C-2	Sequence 2, Appl
38	21	67.7	17	4	US-08-896-933-2	Sequence 2, Appl
39	21	67.7	17	4	US-08-896-933-8	Sequence 8, Appl
40	21	67.7	17	4	US-08-896-933-10	Sequence 10, Appl
41	21	67.7	17	4	US-09-314-235-2	Sequence 2, Appl
42	21	67.7	17	4	US-09-314-235-8	Sequence 8, Appl
43	21	67.7	17	4	US-09-314-235-10	Sequence 10, Appl
44	21	67.7	24	3	US-08-838-413A-4	Sequence 4, Appl
45	21	67.7	24	3	US-08-838-413A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-896-933-6
; Sequence 6, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896, 933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252, 978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-6
Query Match 74.2%; Score 23; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.86;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 KXXXTXQEXD 10
DB 1 KKSVAQELD 10
RESULT 2
US-09-314-235-6
; Sequence 6, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314, 235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896, 933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252, 978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891, 718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466, 577

EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 17
TYPE: PRT
ORGANISM: Staphylococcus aureas
US-09-314-235-6

Query Match 74.2% Score 23; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.86;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
| | | | |
DB 1 KSVTAQELD 10

RESULT 3
US-08-838-413A-20

Sequence 20, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-20

Query Match 74.2% Score 23; DB 3; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
| | | | |
DB 1 KSVTAQELD 10

RESULT 4
US-08-896-933-28

Sequence 28, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 238
TYPE: PRT
ORGANISM: Staphylococcus aureas
US-08-896-933-28

Query Match 74.2% Score 23; DB 4; Length 238;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
| | | | |
DB 150 KSVTAQELD 159

RESULT 5
US-09-314-235-28

Sequence 28, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 238
TYPE: PRT
ORGANISM: Staphylococcus aureas
US-09-314-235-28

Query Match 74.2% Score 23; DB 4; Length 238;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
| | | | |
DB 150 KSVTAQELD 159

RESULT 6


```
US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Staphylococcus aureas
US-08-896-933-27

Query Match          74.2%; Score 23; DB 4; Length 239;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 151 KKSVAQELD 160

RESULT 7
US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Staphylococcus aureas
US-09-314-235-27

Query Match          74.2%; Score 23; DB 4; Length 239;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 151 KKSVAQELD 160

RESULT 8
US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332
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GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match          74.2%; Score 23; DB 4; Length 266;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 178 KKSVAQELD 187

RESULT 9
US-08-896-933-4
; Sequence 4, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRF
; ORGANISM: Staphylococcus aureas
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US-08-896-933-4

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKNVTAQELD 10

RESULT 10

US-08-896-933-12
Sequence 12, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 17
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-08-896-933-12

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKNVTAQELD 10

RESULT 11

US-08-896-933-14
Sequence 14, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 17
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-14

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKNVTAQELD 10

RESULT 12

US-08-896-933-15
Sequence 15, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 17
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-15

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKNVTAQELD 10

RESULT 13

US-08-896-933-16
Sequence 16, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 17
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-16

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKNVTAQELD 10

RESULT 14

US-08-896-933-17
Sequence 17, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
;; FILE REFERENCE: 09629/005002
;; CURRENT APPLICATION NUMBER: US/08/896,933
;; CURRENT FILING DATE: 1997-07-18
;; EARLIER APPLICATION NUMBER: 08/252,978
;; EARLIER FILING DATE: 1994-06-02
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 17
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Other
;; FEATURE:
;; OTHER INFORMATION: Consensus sequences derived from staphylococcus
;; OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-17

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | | |
Db 1 KKNVTQELD 10

RESULT 15
US-09-314-235-4
;; Sequence 4, Application US/09314235
;; Patent No. 6338845
;; GENERAL INFORMATION:
;; APPLICANT: Tezcan, David S.
;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
;; FILE REFERENCE: 09629/005004
;; CURRENT APPLICATION NUMBER: US/09/314,235
;; CURRENT FILING DATE: 1999-05-18
;; EARLIER APPLICATION NUMBER: 08/896,933
;; EARLIER FILING DATE: 1997-07-18
;; EARLIER APPLICATION NUMBER: 08/252,978
;; EARLIER FILING DATE: 1994-06-02
;; EARLIER APPLICATION NUMBER: 07/891,718
;; EARLIER FILING DATE: 1992-06-01
;; EARLIER APPLICATION NUMBER: US91/00342
;; EARLIER FILING DATE: 1991-01-17
;; EARLIER APPLICATION NUMBER: 07/466,577
;; EARLIER FILING DATE: 1990-01-17
;; EARLIER APPLICATION NUMBER: 07/416,530
;; EARLIER FILING DATE: 1989-10-03
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-314-235-4

Query Match 71.0%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | | |
Db 1 KKNVTQELD 10

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:01 ; Search time 12.1212 Seconds
(without alignments)
85.173 Million cell updates/sec

Title: US-09-150-947f-13
Perfect score: 31
Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	74.2	29	10 US-09-864-761-43487	Sequence 43487, A
2	23	74.2	266	1 US-08-882-431-14	Sequence 14, Appl
3	23	74.2	266	9 US-09-870-759-12	Sequence 12, Appl
4	23	74.2	266	9 US-10-002-784A-14	Sequence 14, Appl
5	22	71.0	10	10 US-09-150-947B-3	Sequence 3, Appl
6	22	71.0	10	10 US-09-150-947B-4	Sequence 4, Appl
7	22	71.0	12	9 US-10-113-809-1	Sequence 1, Appl
8	22	71.0	12	9 US-10-113-809-4	Sequence 4, Appl
9	22	71.0	12	10 US-09-150-947B-2	Sequence 2, Appl
10	22	71.0	13	10 US-09-150-947B-5	Sequence 5, Appl
11	22	71.0	13	10 US-09-150-947B-6	Sequence 6, Appl
12	22	71.0	13	10 US-09-150-947B-11	Sequence 11, Appl
13	22	71.0	14	10 US-09-150-947B-9	Sequence 9, Appl
14	22	71.0	14	10 US-09-150-947B-10	Sequence 10, Appl
15	22	71.0	16	10 US-09-150-947B-7	Sequence 7, Appl
16	22	71.0	26	10 US-09-150-947B-1	Sequence 1, Appl
17	22	71.0	35	10 US-09-150-947B-8	Sequence 8, Appl
18	22	71.0	102	9 US-10-047-260-26	Sequence 26, Appl
19	22	71.0	220	9 US-10-002-784A-26	Sequence 26, Appl

20	22	71.0	239	1	US-08-882-431-10	Sequence 10, Appl
21	22	71.0	239	9	US-10-002-784A-10	Sequence 10, Appl
22	22	71.0	239	10	US-09-150-947B-12	Sequence 12, Appl
23	22	71.0	251	1	US-08-882-431-16	Sequence 16, Appl
24	22	71.0	251	8	US-08-973-391A-13	Sequence 13, Appl
25	22	71.0	251	9	US-10-002-784A-16	Sequence 16, Appl
26	22	71.0	265	1	US-08-882-431-6	Sequence 6, Appl
27	22	71.0	265	1	US-08-882-431-8	Sequence 8, Appl
28	22	71.0	266	9	US-09-870-759-10	Sequence 10, Appl
29	22	71.0	266	9	US-10-002-784A-6	Sequence 6, Appl
30	22	71.0	266	9	US-10-002-784A-8	Sequence 8, Appl
31	22	71.0	266	9	US-10-151-336-8	Sequence 8, Appl
32	22	71.0	295	10	US-09-815-242-13351	Sequence 13351, A
33	22	71.0	295	10	US-09-815-242-13691	Sequence 13691, A
34	22	71.0	344	9	US-10-201-310-3	Sequence 3, Appl
35	22	71.0	350	9	US-09-972-473-38	Sequence 38, Appl
36	22	71.0	468	9	US-10-002-784A-27	Sequence 27, Appl
37	22	71.0	659	9	US-10-102-627-74	Sequence 74, Appl
38	22	71.0	922	10	US-09-879-228-2	Sequence 2, Appl
39	21	67.7	12	9	US-10-113-809-2	Sequence 2, Appl
40	21	67.7	72	9	US-10-144-929-189	Sequence 189, Appl
41	21	67.7	177	9	US-10-092-849-5	Sequence 5, Appl
42	21	67.7	177	10	US-09-730-617-95	Sequence 95, Appl
43	21	67.7	190	9	US-09-738-626-4637	Sequence 4637, Appl
44	21	67.7	203	9	US-09-900-766-5	Sequence 5, Appl
45	21	67.7	217	9	US-09-900-766-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-864-761-43487
Sequence 43487, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmlca-X-1
CURRENT APPLICATION NUMBER: US/09/864, 761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43487
LENGTH: 29
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006299.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66
OTHER INFORMATION: EST_HUMAN HIT: AV703706.1, EVALU6 6.00e+00
US-09-864-761-43487

Query Match 74.2%; Score 23; DB 10; Length 29;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
DB 10 KALSTGOEID 19

RESULT 2
US-08-882-431-14
Sequence 14, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC - 504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DERRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266

TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match 74.2%; Score 23; DB 1; Length 266;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
DB 178 KXSVTAQOELD 187

RESULT 3
US-09-870-759-12
Sequence 12, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-12

Query Match 74.2%; Score 23; DB 9; Length 266;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
DB 178 KXSVTAQOELD 187

RESULT 4
US-10-002-784A-14
Sequence 14, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 14
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 74.2%; Score 23; DB 9; Length 266;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXOEXD 10
DB 178 KXSVTAQOELD 187

Db 178 KKSVAQELD 187

RESULT 5

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US-09-150-947B-3
; Sequence 3, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Atad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-3

```

Query Match

Best Local Similarity 71.0%; Score 22; DB 10; Length 10;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTQXEND 10
 Db 1 KKKVTAQELD 10

RESULT 6

```

US-09-150-947B-4
; Sequence 4, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Atad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-4

```

Query Match

Best Local Similarity 71.0%; Score 22; DB 10; Length 10;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTQXEND 10
 Db 1 KKKVTAQELD 10

RESULT 7

```

US-10-113-809-1
; Sequence 1, Application US/10113809
; Patent No. US2002017753A1

```

GENERAL INFORMATION:

```

; APPLICANT: Maschke, Hans, E.
; TITLE OF INVENTION: EXOTOXIN-LIGAND
; FILE REFERENCE: MBP-011XX
; CURRENT APPLICATION NUMBER: US/10/113,809
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 101 16 042.9-41
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacterial Toxin Binding Ligand
US-10-113-809-1

```

Query Match

Best Local Similarity 71.0%; Score 22; DB 9; Length 12;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTQXEND 10
 Db 3 KKKVTAQELD 12

RESULT 8

```

US-10-113-809-4
; Sequence 4, Application US/10113809
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Maschke, Hans, E.
; TITLE OF INVENTION: EXOTOXIN-LIGAND
; FILE REFERENCE: MBP-011XX
; CURRENT APPLICATION NUMBER: US/10/113,809
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 101 16 042.9-41
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacterial Toxin Binding Ligand
US-10-113-809-4

```

Query Match

Best Local Similarity 71.0%; Score 22; DB 9; Length 12;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTQXEND 10
 Db 3 KKKVTAQELD 12

RESULT 9

```

US-09-150-947B-2
; Sequence 2, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Atad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938

```

;; PRIOR FILING DATE: 1996-12-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-150-947B-2

Query Match 71.0%; Score 22; DB 10; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | | |
DB 3 KKKATVQELD 12

RESULT 10
US-09-150-947B-5

;; Sequence 5, Application US/09150947B
;; Patent No. US20020028211A1
;; GENERAL INFORMATION:
;; APPLICANT: Kaempfer, Raymond
;; APPLICANT: Arad, Gila
;; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
;; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
;; FILE REFERENCE: A31967-PCT-USA-A
;; CURRENT APPLICATION NUMBER: US/09/150,947B
;; CURRENT FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
;; PRIOR FILING DATE: 1997-12-30
;; PRIOR APPLICATION NUMBER: ISRAEL 119938
;; PRIOR FILING DATE: 1996-12-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
;; FEATURE:
;; NAME/KEY: LIPID
;; LOCATION: (1)...(1)
;; OTHER INFORMATION: N-lauryl cysteine residue
US-09-150-947B-5

Query Match 71.0%; Score 22; DB 10; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | | |
DB 4 KKKYTAQELD 13

RESULT 11
US-09-150-947B-6

;; Sequence 6, Application US/09150947B
;; Patent No. US20020028211A1
;; GENERAL INFORMATION:
;; APPLICANT: Kaempfer, Raymond
;; APPLICANT: Arad, Gila
;; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
;; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
;; FILE REFERENCE: A31967-PCT-USA-A
;; CURRENT APPLICATION NUMBER: US/09/150,947B
;; CURRENT FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
;; PRIOR FILING DATE: 1997-12-30
;; PRIOR APPLICATION NUMBER: ISRAEL 119938
;; PRIOR FILING DATE: 1996-12-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 6
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
;; FEATURE:
;; NAME/KEY: LIPID
;; LOCATION: (1)...(1)
;; OTHER INFORMATION: N-lauryl cysteine residue
US-09-150-947B-6

Query Match 71.0%; Score 22; DB 10; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | | |
DB 4 KKKATVQELD 13

RESULT 12
US-09-150-947B-11

;; Sequence 11, Application US/09150947B
;; Patent No. US20020028211A1
;; GENERAL INFORMATION:
;; APPLICANT: Kaempfer, Raymond
;; APPLICANT: Arad, Gila
;; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
;; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
;; FILE REFERENCE: A31967-PCT-USA-A
;; CURRENT APPLICATION NUMBER: US/09/150,947B
;; CURRENT FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
;; PRIOR FILING DATE: 1997-12-30
;; PRIOR APPLICATION NUMBER: ISRAEL 119938
;; PRIOR FILING DATE: 1996-12-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 11
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
;; FEATURE:
;; NAME/KEY: ACETYLATION
;; LOCATION: (1)...(1)
;; OTHER INFORMATION: N-acetyl group
;; NAME/KEY: MOD_RES
;; LOCATION: (13)...(13)
;; OTHER INFORMATION: D-alanine
US-09-150-947B-11

Query Match 71.0%; Score 22; DB 10; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | | |
DB 3 KKKATVQELD 12

RESULT 13
US-09-150-947B-9

;; Sequence 9, Application US/09150947B
;; Patent No. US20020028211A1
;; GENERAL INFORMATION:
;; APPLICANT: Kaempfer, Raymond
;; APPLICANT: Arad, Gila
;; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
;; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
;; FILE REFERENCE: A31967-PCT-USA-A
;; CURRENT APPLICATION NUMBER: US/09/150,947B
;; CURRENT FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
;; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (1)...(1)
; NAME/KEY: DISULFID
; LOCATION: (14)...(14)
US-09-150-947B-9

Query Match 71.0%; Score 22; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 6;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 4 KKKATVQELD 13

RESULT 14
US-09-150-947B-10
; Sequence 10, Application US/09150947B
; Patent No. US2002028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)...(1)
; OTHER INFORMATION: D-alanine
; NAME/KEY: MOD_RES
; LOCATION: (14)...(14)
; OTHER INFORMATION: D-alanine
US-09-150-947B-10

Query Match 71.0%; Score 22; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 6;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 4 KKKATVQELD 13

RESULT 15
US-09-150-947B-7
; Sequence 7, Application US/09150947B
; Patent No. US2002028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; TITLE OF INVENTION: ANTAGONISTS AND VACCINES

; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-7

Query Match 71.0%; Score 22; DB 10; Length 16;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 3 KKKATVQELD 12

Search completed: June 5, 2003, 15:49:02
Job time: 13.1212 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:24:01 ; Search time 9.84848 seconds
(without alignments)
97.613 Million cell updates/sec

Title: US-09-150-947F-13

Perfect score: 31

Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	77.4	549	2 E86337	hypothetical prote
2	24	77.4	602	1 RRNZP3	polymerase-associ
3	24	77.4	603	1 RRNZP5	polymerase-associ
4	24	77.4	604	1 RRNZP4	polymerase-associ
5	23	74.2	266	1 ENSAC1	enterotoxin C-1 pr
6	23	74.2	266	2 A60114	enterotoxin C-2 pr
7	23	74.2	266	2 S11885	enterotoxin C3 - S
8	23	74.2	565	2 A87694	ribosomal protein
9	23	74.2	565	2 AB3061	30S ribosomal prot
10	23	74.2	568	1 R3ZRL1	ribosomal protein
11	23	74.2	572	1 E98225	30S ribosomal prot
12	23	74.2	586	1 ORXLE	estrogen receptor
13	23	74.2	3212	2 T24692	hypothetical prote
14	22	71.0	102	2 S74843	hypothetical prote
15	22	71.0	136	2 A89969	enterotoxin YEMT2
16	22	71.0	184	2 F86681	prophage pil prote
17	22	71.0	236	2 S18789	exotoxin A precurs
18	22	71.0	236	2 S18786	exotoxin type A pr
19	22	71.0	236	2 S18783	exotoxin type A pr
20	22	71.0	239	2 D89969	enterotoxin SEM [1
21	22	71.0	240	2 G89991	extracellular ente
22	22	71.0	242	2 C89969	extracellular ente
23	22	71.0	247	2 T22335	hypothetical prote
24	22	71.0	251	1 S29659	exotoxin type A pr
25	22	71.0	251	1 QOECF	Replication initia
26	22	71.0	258	2 H89968	enterotoxin Sen [1
27	22	71.0	260	2 E89969	enterotoxin Sen [1
28	22	71.0	266	1 ENSAB6	enterotoxin B prec
29	22	71.0	295	2 D95107	hypothetical prote

30	22	71.0	295	2 F97975	hypothetical prote
31	22	71.0	332	1 DEBYG2	glyceraldhyde-3-P
32	22	71.0	333	2 JC5787	ribonuclease H (EC
33	22	71.0	356	2 T38408	hypothetical prote
34	22	71.0	520	2 G71647	hypothetical prote
35	22	71.0	523	2 F97865	hypothetical prote
36	22	71.0	672	2 F71424	hypothetical prote
37	22	71.0	835	2 T05259	probable disease r
38	22	71.0	886	2 T39229	hypothetical prote
39	22	71.0	922	2 T37292	hypothetical prote
40	22	71.0	946	2 A84133	DNA ligase (ATP) (
41	22	71.0	1146	2 H96796	hypothetical prote
42	22	71.0	1200	2 S77524	chromosome segrega
43	22	71.0	1314	2 A85176	hypothetical prote
44	22	71.0	1327	2 D70759	probable ocsb prot
45	22	71.0	1738	2 T14867	interactin - slime

ALIGNMENTS

RESULT 1
E86337
hypothetical protein F14010.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86337
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-549 <STO>
A:Cross-references: GB:AE005172; NID:99558589; PIDN:AAF88152.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
Query Match 77.4% Score 24; DB 2; Length 549;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 KXXXTXQEXD 10
Db 27 KISTGQEND 36
RESULT 2
RRNZP3
polymerase-associated nucleocapsid phosphoprotein - parainfluenza virus type 3 (strat
C:Species: parainfluenza virus type 3
C:Accession: A27010
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Jul-1997
R:Spriggs, M.K.; Collins, P.L.
J. Gen. Virol. 67, 2705-2719, 1986
A:Title: Sequence analysis of the P and C protein genes of human parainfluenza virus
A:Reference number: A92793; MUID:87085488; PMID:3025346
A:Accession: A27010
A:Molecule type: mRNA
A:Residues: 1-602 <SPR>
C:Comment: This protein may be a component of the active polymerase.
C:Genetics:
A:Gene: P
C:Superfamily: parainfluenza virus polymerase-associated nucleocapsid phosphoprotein

C:Keywords: nucleocapsid; phosphoprotein

Query Match 77.4%; Score 24; DB 1; Length 602;
Best Local Similarity 50.0%; Pred. NO. 68;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 226 KSSSTHQEDD 235

RESULT 3

RNNZ5
polymerase-associated nucleocapsid phosphoprotein (version 2) - parainfluenza virus type

C:Species: parainfluenza virus type 3
A:Note: host: Homo sapiens (man)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 24-Jul-1997

C:Accession: A26896
R:Galinski, M.S.; Mink, M.A.; Lambert, D.M.; Wechsler, S.L.; Pons, M.W.
Virology 155, 46-60, 1986

A:Title: Molecular cloning and sequence analysis of the human parainfluenza 3 virus mRNA
A:Reference number: A94348; MUID:87044104; PMID:3022477
A:Accession: A26896

A:Molecule type: mRNA
A:Residues: 1-603 <GAL>

C:Comment: The RNA sequence was obtained from GenBank, release 52.0.
C:Comment: This protein may be a component of the active polymerase.

C:Genetics:

A:Gene: P
C:Superfamily: parainfluenza virus polymerase-associated nucleocapsid phosphoprotein
C:Keywords: nucleocapsid; phosphoprotein

Query Match 77.4%; Score 24; DB 1; Length 603;
Best Local Similarity 50.0%; Pred. NO. 68;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 226 KSSSTHQEDD 235

RESULT 4

RNNZ4
polymerase-associated nucleocapsid phosphoprotein (version 1) - parainfluenza virus type

C:Species: parainfluenza virus type 3
A:Note: host: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Jul-1997

C:Accession: A94355; A24189
R:Luk, D.; Sanchez, A.; Banerjee, A.K.
Virology 156, 193-194, 1987

A:Reference number: A94355
A:Contents: erratum
A:Accession: A94355

A:Molecule type: mRNA
A:Residues: 1-604 <LUI>

A:Cross-references: GB:M14890
R:Luk, D.; Sanchez, A.; Banerjee, A.K.
Virology 153, 318-325, 1986

A:Title: Messenger RNA encoding the phosphoprotein (P) gene of human parainfluenza virus
A:Reference number: A94343; MUID:86291173; PMID:3016995
A:Accession: A24189

A:Molecule type: mRNA
A:Residues: 1-603; AKDQIKTTPNK' <LUI>

A:Note: this sequence has been corrected in reference A94355
C:Comment: This protein may be a component of the active polymerase.

C:Genetics:

A:Gene: P
C:Superfamily: parainfluenza virus polymerase-associated nucleocapsid phosphoprotein
C:Keywords: nucleocapsid; phosphoprotein

Query Match 77.4%; Score 24; DB 1; Length 604;
Best Local Similarity 50.0%; Pred. NO. 69;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 226 KSSSTHQEDD 235

RESULT 5

ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999

C:Accession: S06356; A01816
R:Bohach, G.A.; Schlievert, P.M.

Mol. Gen. Genet. 209, 15-20, 1987
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness

A:Reference number: S06356; MUID:88038352; PMID:2823067
A:Accession: S06356

A:Molecule type: DNA
A:Residues: 1-266 <BOH>

A:Cross-references: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R:Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983

A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A:Reference number: A01816; MUID:83213327; PMID:6189824

A:Molecule type: protein
A:Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>

C:Genetics:

A:Gene: entC1
C:Superfamily: enterotoxin B

C:Keywords: enterotoxin
E:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-1 #status experimental <MAT>

F:120-137/Dissulfide bonds: #status experimental

Query Match 74.2%; Score 23; DB 1; Length 266;
Best Local Similarity 50.0%; Pred. NO. 55;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 178 KSVTAQELD 187

RESULT 6

A60114
enterotoxin C-2 precursor - Staphylococcus aureus

N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999

C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotox

A:Reference number: A60114; MUID:89277549; PMID:2543637
A:Accession: A60114

A:Molecule type: not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-266 <BOH>
A:Accession: B60114

A:Molecule type: protein
A:Residues: 28-66 <BOH2>

R:Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989

A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests

A:Reference number: A33866; MUID:89327174; PMID:2473979
A:Accession: A33866

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-266 <COU>
A:Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004

C:Genetics:

A:Gene: entC2

C:Superfamily: enterotoxin B
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 74.2% Score 23; DB 2; Length 266;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 178 KKSXTAQELD 187

RESULT 7

S11885 enterotoxin C3 - Staphylococcus aureus

C:Species: Staphylococcus aureus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C:Accession: S11885
R:Hoyle, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison
A:Reference number: S11885; MID:90220508; PMID:2325627

A:Accession: S11885
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <HOV>
A:Cross-references: GB:AE005673; MID:946570; PIDN:CAA35972.1; PID:946571
C:Superfamily: enterotoxin B

Query Match 74.2% Score 23; DB 2; Length 266;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 178 KKSXTAQELD 187

RESULT 8

A87694 ribosomal protein S1 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: A87694

R:Merz, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MID:21173698; PMID:11259647

A:Accession: A87694
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-565 <STO>
A:Cross-references: GB:AE005673; MID:913425331; PIDN:AAK25549.1; GSPDB:GN00148
C:Gene: CC3587
C:Superfamily: Escherichia coli ribosomal protein S1

Query Match 74.2% Score 23; DB 2; Length 565;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 326 KIVSTSQEVD 335

RESULT 9

AB3061 30S ribosomal protein S1 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AB3061
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woerger, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McCluskey, K.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamster, E.W.

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AB3061

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-566 <KUR>

A:Cross-references: GB:AE008689; PIDN:AA44904.1; PID:917742555; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Gene: rpsA

A:Map position: linear chromosome

C:Superfamily: linear chromosome

Query Match 74.2% Score 23; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 326 KIVSTSQEVD 335

RESULT 10

R32R1 ribosomal protein S1 - Rhizobium meliloti

C:Species: Rhizobium meliloti
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C:Accession: S01055

R:Schneider, J.; Thamm, S.; Lutz, R.; Hussain, A.; Faist, G.; Dobrinski, B.

Nucleic Acids Res. 16, 3075-3089, 1988

A:Title: Cloning and characterization of a gene from Rhizobium meliloti 2011 coding

A:Reference number: S01055; MID:88217521; PMID:3368316

A:Accession: S01055

A:Molecule type: DNA

A:Residues: 1-568 <SCH>

A:Cross-references: EMBL:X07528; MID:946338; PIDN:CAA30404.1; PID:946339

A>Note: the sequence from Fig. 5 is inconsistent with that from Fig. 4 in having 565-

C:Gene: rpsA

C:Superfamily: Escherichia coli ribosomal protein S1

C:Keywords: duplication; protein biosynthesis; ribosome; RNA binding

F:196-453/Domain: RNA binding #status predicted <RNA>

F:196-279,280-366,367-453/Region: duplication

Query Match 74.2% Score 23; DB 1; Length 568;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
DB 326 KIVSTSQEVD 335

RESULT 11

E98225 30S ribosomal protein S1 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C:Species: Agrobacterium tumefaciens

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002

C:Accession: E98225

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ounoljo, B.; Gold

A: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: E98225

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-572 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK89327.1; PID:g15159167; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR.L1496
 A:Map position: linear chromosome
 C:Superfamily: Escherichia coli ribosomal protein S1

Query Match 74.2% Score 23; DB 2; Length 572;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 332 KILSTQEXD 341

RESULT 12

ORXLE

estrogen receptor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 15-Jun-1996
 C:Accession: A40907

R:Weller, I.J.; Lew, D.; Shapiro, D.J.

Mol. Endocrinol. 1, 355-362, 1987

A:Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian re
 A:Reference number: A40907; MUID:90331927; PMID:3274894
 A:Accession: A40907

A:Molecule type: mRNA

A:Residues: 1-586 <MEI>

A:Cross-references: GB:L20735

C:Comment: The steroid hormones and their receptors are involved in the regulation of eu
 C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
 C:Comment: complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
 C:Superfamily: estrogen receptor; erba transforming protein homology
 C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
 F:1-174/Domain: amino-terminal <NH2>
 F:175-266/Domain: DNA binding #status predicted <DNA>
 F:178-448/Domain: erba transforming protein homology <ERBA>
 F:178-201/Region: zinc finger CCCC motif
 F:214-237/Region: zinc finger CCCC motif
 F:251-266/Region: nuclear location signal
 F:292-544/Domain: steroid binding #status predicted <STB>
 F:180,183,197,200/Binding site: zinc (Cys) #status predicted
 F:216,222,232,235/Binding site: zinc (Cys) #status predicted
 F:231/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 74.2% Score 23; DB 1; Length 586;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 545 KDKTTQEXD 554

RESULT 13

T24692

hypothetical protein T08G11.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T24692

R:Dobson, R.

submitted to the EMBL Data Library, September 1996

A:Reference number: Z19925

A:Accession: T24692

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-3212 <WIL>

A:Cross-references: EMBL:Z80220; PIDN:CAB02304.1; GSPDB:GN00019; CESP:T08G11.1
 A:Experimental source: clone T08G11
 C:Genetics:

A:Gene: CESP:T08G11.1
 A:Map position: 1
 A:Introns: 34/1; 149/3; 182/3; 527/2; 766/1; 1070/3; 1769/3; 1834/3; 2070/2; 2210/3;

Query Match 74.2% Score 23; DB 2; Length 3212;
 Best Local Similarity 50.0%; Pred. No. 8e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 2264 KSVTQEXD 2273

RESULT 14

S74843

hypothetical protein s110846 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S74843

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima,
 O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
 DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
 S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74843

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <KAN>

A:Cross-references: EMBL:D90909; GB:AB001339; NID:g1653844; PIDN:BA17804.1; PID:g101

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 71.0% Score 22; DB 2; Length 102;
 Best Local Similarity 50.0%; Pred. No. 38;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 72 KKKTKQEXD 81

RESULT 15

A89969

enterotoxin YEMT2 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: A89969

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: A89969

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KUR>

A:Cross-references: GB:BA000018; PID:g13701619; PIDN:BA842912.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: yent2

Query Match 71.0% Score 22; DB 2; Length 136;
 Best Local Similarity 50.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 50 KKNITQEXD 59

Search completed: June 5, 2003, 15:33:57

Fri Jun 6 09:14:29 2003

Job time : 13.8485 secs

us-09-150-947f-13.rpr

Page 5

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:34:07 ; Search time 6.51515 Seconds
(without alignments)
63.661 Million cell updates/sec

Title: US-09-150-947F-13

Perfect score: 31

Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	77.4	604	RRPP_P13H4	P06162 human para
2	74.2	266	ETC1_STAAU	P01553 staphylococ
3	74.2	266	ETC2_STAAU	P34071 staphylococ
4	74.2	266	ETC3_STAAU	P23313 staphylococ
5	74.2	568	RSL_RHIME	P14129 rhizobium m
6	74.2	586	ESR1_XENLA	P81559 xenopus lae
7	71.0	251	REEL_ECOLI	P03856 escherichia
8	71.0	251	SPRA_STRPY	P08095 streptococ
9	71.0	266	ETXB_STAAU	P01552 staphylococ
10	71.0	331	G3P3_YEAST	P00359 saccharomyc
11	71.0	350	DKR3_CHICK	P00839 gallus gall
12	71.0	356	YDGC_SCHPO	O10498 schizosacch
13	71.0	520	Y855_RICPR	O92ca5 rickettsia
14	71.0	712	ANS2_CABEL	O96615 caenorhabdl
15	71.0	886	YE86_SCHPO	O14302 schizosacch
16	71.0	922	DNL3_HUMAN	P49916 homo sapien
17	71.0	1015	DNL3_MOUSE	P97866 mus musculu
18	71.0	1327	YK06_MYCTU	O10850 mycobacteri
19	67.7	176	YRS9_LISMO	O8y883 listeria mo
20	67.7	177	ILIX_HORSE	O18899 equus cabal
21	67.7	228	GLI_ARATH	P27900 arabidopsis
22	67.7	234	SPGC_STRPY	O9xsc7 streptococ
23	67.7	235	SPEC_STRPY	P13380 streptococ
24	67.7	236	SPER_STRPY	O9xsc8 streptococ
25	67.7	257	ETXA_STAAU	P13163 staphylococ
26	67.7	257	ETXE_STAAU	P12993 staphylococ
27	67.7	258	ETXD_STAAU	P20723 staphylococ
28	67.7	258	ETYG_STAAU	O85382 staphylococ
29	67.7	276	PYGI_SYNEL	P50039 synecococc
30	67.7	283	YJ81_YEAST	P47148 saccharomyc
31	67.7	351	PEXE_PICAN	P78723 pichia angu
32	67.7	375	NPLA_HUMAN	O99733 homo sapien
33	67.7	385	TGT_ZYMO	P28720 zymomonas m

34	21	67.7	461	1	DISK_MOUSE	O61466 mus musculu
35	21	67.7	480	1	SYP_MYCLE	O92517 mycobacteri
36	21	67.7	554	1	NBLA_MOUSE	P52963 mus musculu
37	21	67.7	684	1	FLID_HELPJ	O92191 helicobacte
38	21	67.7	684	1	FLID_HELPJ	P96786 helicobacte
39	21	67.7	727	1	GPM_HUMAN	P43304 homo sapien
40	21	67.7	727	1	GPM_MOUSE	O64521 mus musculu
41	21	67.7	899	1	ANDR_MOUSE	P19091 mus musculu
42	21	67.7	904	1	NIA1_TOBAC	P11605 nicotiana t
43	21	67.7	904	1	NIA2_TOBAC	P08509 nicotiana t
44	21	67.7	1184	1	XMS2_DROME	O9u3v9 drosophila
45	21	67.7	1305	1	GAK_RAT	P97874 rattus norv

ALIGNMENTS

RESULT 1
ID RRP_P13H4 STANDARD; PRT; 604 AA.
AC P06162;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid phosphoprotein).
GN P.
OS Human parainfluenza 3 virus (strain NIH 47885).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX NCBI_TaxID=11217;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86291173; PubMed-3016995;
RA Luk D., Sanchez A., Banerjee A.K.;
RT "Messenger RNA encoding the phosphoprotein (P) gene of human parainfluenza virus 3 is bicistronic."
RL Virology 153:318-325(1986).
RN [2]
RP REVISIONS.
RA Luk D., Sanchez A., Banerjee A.K.;
RL Virology 156:193-194(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-87044104; PubMed-3022477;
RA Gallinski M.S., Mink M.A., Lambert D.M., Wechsler S.L., Pons W.M.;
RT "Molecular cloning and sequence analysis of the human parainfluenza 3 virus mRNA encoding the P and C proteins."
RL Virology 155:46-60(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-87085488; PubMed-3025346;
RA Spriggs M.K., Collins P.L.;
RT "Sequence analysis of the P and C protein genes of human parainfluenza virus type 3: patterns of amino acid sequence homology among paramyxovirus proteins."
RL J. Gen. Virol. 67:2705-2719(1986).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate + (RNA)(N).
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CC EMBL: M14890; AAA6866.1; ALT-SEQ.
CC DR X04721; CAA28429.1; -
CC EMBL: M14932; AAA6818.1; -

DR EMBL: D10029; BA00921.1; ALT_SEQ.
 DR PIR: A27010; RRN2P3.
 DR PIR: A24189; RRN2P4.
 DR PIR: A26896; RRN2P5.
 DR InterPro: IPR002693; Paramyxo_P.
 DR Pfam: PF01806; Paramyxo_P.1.
 DR Transferase; RNA-directed RNA polymerase: Nucleocapsid;
 KM Phosphorylation.
 FT CONFLICT 198 198 P -> N (IN REF. 4).
 FT CONFLICT 243 243 MISSING (IN REF. 3 AND 4).
 FT CONFLICT 244 244 MISSING (IN REF. 4).
 FT CONFLICT 316 316 Q -> R (IN REF. 3).
 FT CONFLICT 584 584 C -> S (IN REF. 4).
 SQ SEQUENCE 604 AA; 67661 MW; D2E06EF47027D0BD CRC64;
 Query Match 77.4%; Score 24; DB 1; Length 604;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXQEXD 10
 Db 226 KXSSTHOEDD 235

RESULT 2

ETC1_STRAU STANDARD; PRT; 266 AA.
 AC P01553;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-1 precursor (SEC1).
 GN EMTC1.
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88038352; PubMed=2823067;
 RA Bohach G.A., Schlievert P.M.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
 RL relatedness to other pyrogenic toxins.";
 RL Mol. Gen. Genet. 209:15-20(1987).
 RN [2]
 RP SEQUENCE OF 28-266.
 RX MEDLINE=83213327; PubMed=6189824;
 RA Schmidt J.J., Spero L.;
 RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
 RL J. Biol. Chem. 258:6300-6306(1983).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC
 DR EMBL: X05815; CAA29260.1; -
 DR PIR: A01816; ENSAC1.
 DR PIR: S06356; S06356.
 DR HSSP: P34071; 1SE2.
 DR InterPro: IPR001961; Stap/Strep_toxin.
 DR Pfam: PF01123; Stap_stp_toxin; 1.
 DR Pfam: PF02876; Stap_stp_tox_C; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
 FT DISULFID 120 137
 FT CONFLICT 177 177 D -> N (IN REF. 2).
 SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A898653B CRC64;
 Query Match 74.2%; Score 23; DB 1; Length 266;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXQEXD 10
 Db 178 KKSVAQELD 187

RESULT 3

ETC2_STRAU STANDARD; PRT; 266 AA.
 AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN EMTC2.
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 RL enterotoxins C1 and C2.";
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RL staphylococcus aureus reveals a zinc-binding site.";
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RL enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RL enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- CORACOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC
 DR PIR: A60114; A60114.
 DR PDB: 1SE2; 23-DEC-96.
 DR PDB: 1SE2; 08-MAR-96.
 DR InterPro: IPR001961; Stap/Strep_toxin.
 DR Pfam: PF01123; Stap_stp_toxin; 1.
 DR Pfam: PF02876; Stap_stp_tox_C; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 RM 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 74.2%; Score 23; DB 1; Length 266;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KKKXTQXEND 10
 DB 178 KKSVAQELD 187

RESULT 4
 ETC3_STAM STANDARD; PRT; 266 AA.
 ID ETC3_STAM
 AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN ETC3 OR SAV2009 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mu50 / ATCC 700699, and N315;
 RX MEDLINE-21311952; PubMed-11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratsugu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90220508; PubMed-2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 sequence comparison of all three type C staphylococcal
 enterotoxins";
 RL Mol. Gen. Genet. 220:329-333(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE-97064178; PubMed-8906797;
 RA Fields B.A., Melchiodi E.L., Li H., Yeern X., Stauffacher C.V.,
 RA Schlievert P.M., Karjalainen K., Maritzuza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 superantigen";
 RL Nature 384:188-192(1996).
 RN [4]
 RP SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 CC EMBL: AP003364; BAB58171.1; -
 CC EMBL: AP003364; BAB58171.1; -
 CC EMBL: X51661; CA35972.1; -
 CC PIR: S11885; S11885.
 CC PDB: 1JCK; 12-NOV-97.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_toxin_C; 1.
 DR PRINTS: PR00279; BACSTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
 KM Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137
 SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;

Query Match 74.2%; Score 23; DB 1; Length 266;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KKKXTQXEND 10
 DB 178 KKSVAQELD 187

RESULT 5
 RSL_RHIME STANDARD; PRT; 568 AA.
 ID RSL_RHIME
 AC P14129;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S1.
 GN RPSA OR R00255 OR SMC00335.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RCR2011 / SU47;
 RX MEDLINE-88217521; PubMed-3368316;
 RA Schindler J., Thamm S., Lutz R., Hussain A., Faist G.,
 RA Dobrinski B.;
 RT "Cloning and characterization of a gene from Rhizobium meliloti 2011
 coding for ribosomal protein S1";
 RL Nucleic Acids Res. 16:3075-3089(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021.
 RX MEDLINE-21396507; PubMed-11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Gohl T., Goffeau A., Kahn D., Kiss E., Leleure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -1- FUNCTION: BINDS mRNA; THUS FACILITATING RECOGNITION OF THE
 CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
 CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
 CC -1- SIMILARITY: CONTAINS 6 SI MOTIF DOMAINS.
 CC -----

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DR EMBL; X07528; CAA30404.1; -
 DR EMBL; AL591783; CAC41692.1; -
 DR PIR; S01055; R3ZRI.
 DR HSSP; P05055; ISRO.
 DR InterPro; IPR000110; Ribosomal_S1.
 DR InterPro; IPR003029; S1.
 DR Pfam; PF00575; S1; 6.
 DR PRINTS; PR00681; RIBOSOMAL_S1.
 DR SMART; SM00316; S1; 6.
 DR TIGRfam; TIGR00717; rpsA; 1.
 DR PROSITE; PS50126; S1; 6.
 KW Ribosomal protein; Repeat; RNA-binding; Complete proteome.
 FT DOMAIN 27 93 S1 MOTIF 1.
 FT DOMAIN 111 177 S1 MOTIF 2.
 FT DOMAIN 198 266 S1 MOTIF 3.
 FT DOMAIN 283 353 S1 MOTIF 4.
 FT DOMAIN 370 440 S1 MOTIF 5.
 FT DOMAIN 459 530 S1 MOTIF 6.
 FT CONFLICT 88 A -> R (IN REF. 1).
 FT CONFLICT 153 162 LMHPDPEI -> ADAPALRN (IN REF. 1).
 FT CONFLICT 235 235 N -> K (IN REF. 1).
 FT CONFLICT 241 241 L -> O (IN REF. 1).
 FT CONFLICT 551 551 A -> R (IN REF. 1).
 SQ SEQUENCE 568 AA; 62640 MW; AB0858204273A7B8 CRC64;

Query Match 74.2%; Score 23; DB 1; Length 568;
 Best Local Similarity 50.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
 | | | | |
 DB 326 KILSTQEVLD 335

RESULT 6
 ID ESRL_XENLA STANDARD; PRT; 586 AA.
 AC P81559;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
 GN ESRL OR NR3A1 OR ESR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_Taxid=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90331927; PubMed=3274894;
 RA Weller I.J., Lew D., Shapiro D.J.;
 RT "The Xenopus laevis estrogen receptor: sequence homology with human
 RT and avian receptors and identification of multiple estrogen receptor
 RT messenger ribonucleic acids."
 RL Mol. Endocrinol. 1:355-362(1987).
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED
 CC IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
 CC CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -1- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 CC BETA (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

CC NR3 SUBFAMILY.

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DR EMBL; L20735; -; NOT_ANNOTATED_CDS.
 DR HSSP; P03372; 1HCQ.
 DR TRANSFAC; T00263; -
 DR InterPro; IPR000536; Hormone_rec_1lg.
 DR InterPro; IPR001292; Oestrgn_receptor.
 DR InterPro; IPR001723; Sthrmn_receptor.
 DR InterPro; IPR001628; Znf_Casteroid.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; Zf-C4; 1.
 DR Pfam; PF02159; Oest_rec; 1.
 DR PRINTS; PR00398; STRDHOMONER.
 DR PRODOM; PD000035; Znf_Casteroid; 1.
 DR SMART; SM00430; HOLY; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding.
 FT DOMAIN 1 179 MODULATING.
 FT DNA_BIND 180 245 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 180 200 C4-TYPE.
 FT ZN_FING 216 240 C4-TYPE.
 FT DOMAIN 246 302 HINGE.
 FT DOMAIN 303 586 STEROID-BINDING.
 SQ SEQUENCE 586 AA; 66080 MW; 0EDC77EBDD6F08BF CRC64;

Query Match 74.2%; Score 23; DB 1; Length 586;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
 | | | | |
 DB 545 KDKTTQEDD 554

RESULT 7
 ID REEL_ECOLI STANDARD; PRT; 251 AA.
 AC P03856; P08969;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Replication initiation protein (REP protein) (Protein E) (F4 protein).
 GN REPE OR REP OR E.
 OS Escherichia coli.
 OX Plasmid F.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82051318; PubMed=7028572;
 RA Murotsu T., Matsubara K., Sugisaki H., Takanami M.;
 RT "Nine unique repeating sequences in a region essential for
 RT replication and incompatibility of the mini-F plasmid."
 RL Gene 15:257-271(1981).
 CC (2)
 RP SEQUENCE FROM N.A.
 RA Eigenlaub R.;
 RT "F plasmid DNA complete mini-F region (F coordinates 40,301F to
 RT 49,869F)." ;
 RL Submitted (Aug-1986) to the EMBL/GenBank/DBJ databases.
 RN [3]

```

RP SEQUENCE FROM N.A.
RC STRAIN-K12 / CR63:
RA Shintzu H., Satoh Y., Suda Y., Dehara K., Sampei G., Mizobuchi K.;
RT "Complete nucleotide sequence of the F plasmid: its implications for
RT organization and diversification of plasmid genomes.";
RL submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 211-251 FROM N.A.
RC MEDLINE-81234554; PubMed-7018695;
RA Tolin A., Helinski D.R.;
RT "Direct repeats of the F plasmid incC region express F
RT incompatibility.";
RL Cell 24:687-694(1981).
RN [5]
RP SEQUENCE OF 1-17 FROM N.A.
RC MEDLINE-86174346; PubMed-3007930;
RA Disque-Kochem C., Seidel U., Helsenberg M., Eichenlaub R.;
RT "The repeated sequences (incB) preceding the protein E gene of
RT plasmid mini-F are essential for replication.";
RL Mol. Gen. Genet. 202:132-135(1986).
RN [6]
RP SEQUENCE OF 209-251 FROM N.A.
RC STRAIN-K12;
RA MEDLINE-87141188; PubMed-3029390;
RA Mori H., Kondo A., Ohshima A., Ogura T., Hiraga S.;
RT "Structure and function of the F plasmid genes essential for
RT partitioning.";
RL J. Mol. Biol. 192:1-15(1986).
RN [7]
RP SIMILARITY: REGIONS OF SIMILARITY WITH REPA PROTEIN OF THE P1
PLASMID, BUT NOT WITH REPLICATION PROTEINS OF OTHER PLASMIDS.
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CC
DR EMBL, J01724; AAA91062.1; -
DR EMBL, M12987; AAA24901.1; -
DR EMBL, AP001918; BAA97915.1; -
DR EMBL, X03410; CAA27146.1; -
DR EMBL, X04619; CAA28294.1; -
DR PIR, A04485; QOECF.
DR PIR, D25783; D25783.
DR Ecogene; EG40058; repe.
DR InterPro: IPR000525; Inlter.RepB.
DR Pfam; PF01051; RepB_protein; 1.
DR Plasmid; DNA replication; Plasmid copy control; Complete proteome.
SQ SEQUENCE 251 AA: 29358 MW: EA2BC65D80158B2 CRC64;
-----
OY Query Match 71.0%; Score 22; DB 1; Length 251;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DB 1 KXXXTXQEXD 10
48 KSDGTLQEHQD 57
-----
RESULT 8
SPEA_STRPY STANDARD; PRT; 251 AA.
AC P08095;
DT 01-AUG-1980 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN SPEA OR SPYMI18_0393.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).

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CC Bacteri: Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus
 CC NCBI_TaxID-1314, 186103;
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86166804; PubMed-3514452;
 RA Weeks C.R., Ferrett J.J.;
 RT "Nucleotide sequence of the type A streptococcal exotoxin
 RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 RT T12.";
 RL Infect. Immun. 52:144-150(1986).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86284313; PubMed-3526093;
 RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 RT related to Staphylococcus aureus enterotoxin B.";
 RL Mol. Gen. Genet. 203:354-356(1986).
 RL [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-WGAS8232 / Serotype M18;
 RC MEDLINE-21927593; PubMed-11917108;
 RA Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Riclefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 RL [4]
 RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
 RX MEDLINE-98094887; PubMed-9678045;
 RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
 RA O'Brien S.M., Tranter H.S., Acharya K.R.;
 RT "Structural basis for the recognition of superantigen streptococcal
 RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
 RT receptors.";
 RL Embo J. 18:9-21(1999).
 RL -1- SUBUNIT: Blnds to major histocompatibility complex class II beta
 chain.
 CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 DR EMBL: U0453; AAC48868.1; -;
 DR EMBL: X0329; CAA27568.1; -;
 DR EMBL, AE009982; AA197141.1; -;
 DR PIR: A26152; A26152.
 DR PIR: S29659; S29659.
 DR PDB: 1B12; 24-NOV-99.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR Pfam: PF00279; BACTRLOXIN.
 DR PRINTS: PRO0279; BACTRLOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 251 EXOTOXIN TYPE A.

FT	DISULFID	117	128	K -> E (IN REF. 2).
FT	CONFLICT	6	6	VT -> MK (IN REF. 2).
FT	CONFLICT	17	18	SQEVPAODPD -> LPKGICTSRPK (IN REF. 2).
FT	CONFLICT	25	35	H -> Q (IN REF. 2).
FT	CONFLICT	40	40	S -> N (IN REF. 2).
FT	CONFLICT	43	43	NLQNIYFEYEGDP -> TFKIYIFMRVTL (IN REF. 2).
FT	CONFLICT	47	59	I -> L (IN REF. 2).
FT	CONFLICT	129	129	TNKKMTVAQELDYK -> QINNGNCRSISYT (IN REF. 2).
FT	CONFLICT	165	178	
SO	SEQUENCE	251 AA;	29246 MM;	54001FEACCBFC3 CRC64;
QY	1 KXXXTXOEXD 10	71.0%;	Score 22;	DB 1;
Dd	167 KKMYTAQELD 176	Best Local Similarity	50.0%;	Pred. NO. 36;
		Matches	5;	Conservative 0;
			Mismatches	5;
			Indels	0;
			Gaps	0.
RESULT 9				
ETXB_STAAU				
ID	ETXB_STAAU	STANDARD;	PRF:	266 AA.
AC	P01552;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Enterotoxin type B precursor (SEB).			
GN	ENTB.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
Ox	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86168029; Pubmed=3957869;			
RT	Jones C.L., Khan S.A.;			
RL	"Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";			
RN	J. Bacteriol. 166:29-33(1986).			
RN	[2]			
RP	SEQUENCE OF 40-91 FROM N.A.			
RX	MEDLINE=85298255; Pubmed=3898073;			
RA	Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;			
RT	"Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).			
RN	[3]			
RP	SEQUENCE OF 28-266 (S-6).			
RX	MEDLINE=71007902; Pubmed=5470821;			
RA	Huang I.-Y., Bergdoll M.S.;			
RT	"The primary structure of staphylococcal enterotoxin B. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";			
RL	J. Biol. Chem. 245:3518-3525(1970).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).			
RX	MEDLINE=93063291; Pubmed=1436058;			
RA	Swaminathan S., Furey W.F., Jr., Pletcher J., Sax M.;			
RT	"Crystal structure of staphylococcal enterotoxin B, a superantigen.";			
RL	Nature 359:801-806(1992).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.			
RX	MEDLINE=94203282; Pubmed=8152483;			
RA	Jardetzky T.S., Brown J.H., Gorge J.C., Stern L.J., Urban R.G.;			
RT	Chen Y.I., Stauffer C., Strominger J.L., Wiley D.C.;			
RL	"Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";			
RL	Nature 368:711-718(1994).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.			
RX	MEDLINE=99096296; Pubmed=9881971;			

```

RA  LI H., Labera A., Tsuchiya D., Leder L., Ysern X., Schliwert P.M.,
RA  Karjalainen K., Maritzuza R.A.:
RA  "Three-dimensional structure of the complex between a T cell receptor
RT  beta chain and the superantigen staphylococcal enterotoxin B."
RL  Immunoty 9:807-816(1998).
RN  (7)
RP  X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX  MEDLINE=98181012; PubMed=9514739.
RA  Papaioeorgiou A.C., Tranter H.S., Acharya K.R.:
RT  "Crystal structure of microbial superantigen staphylococcal
RT  enterotoxin B at 1.5-A resolution. Implications for superantigen
RT  recognition by MHC class II molecules and T-cell receptors."
RL  J. Mol. Biol. 277:61-79(1998).
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC  -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC  FAMILY.
-----
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CC  entities requires a license agreement (see license@sdb.ch">http://www.isb-sdb.ch/announce/
CC  or send an email to license@sdb.ch).
-----
DR  EMBL; M11118; AAA88550.1; -.
DR  PIR; A01815; ENSAB6.
DR  PIR; S27360; S27360.
DR  PDB; 1SEB; 20-JUN-96.
DR  PDB; 2SEB; 28-JAN-98.
DR  PDB; 3SEB; 27-MAY-98.
DR  PDB; 1SE3; 16-JUN-97.
DR  PDB; 1SE4; 15-OCT-97.
DR  PDB; 1SBB; 04-MAR-99.
DR  InterPro; IPR001961; Staph/strep_toxin.
DR  Pfam; PF01123; Staph_strip_toxin.
DR  Pfam; PF02876; Staph_strip_toxin; 1.
DR  PRINTS; PR00279; BACTRUTOXIN.
DR  PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR  PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW  Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT  SIGNAL 1 27
FT  CHAIN 28 266
FT  DISULFID 120 140
FT  CONFICT 56 58
FT  CONFICT 69 77
FT  CONFICT 118 118
FT  CONFICT 128 130
FT  CONFICT 133 135
FT  CONFICT 149 150
FT  CONFICT 156 156
FT  CONFICT 185 186
FT  CONFICT 233 233
FT  CONFICT 246 247
SQ  SEQUENCE 266 AA; 31436 MM; BbD417F61Cf01B80 CXC64;
      1 KXXXTXQEXD 10
      1 1111
Db 179 KKKVTAQELD 188

Query Match 71.0%; Score 22; DB 1; Length 266;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 10
ID G3P3_YEAST
AC P00359;
ID G3P3_YEAST STANDARD; PRT; 331 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

```

15-UTN-2002 (rel. 41, last annotation update)
 DE glyceraldehyde 3-phosphate dehydrogenase 3 (EC 1.2.1.12) (GAPDH 3).
 GN TDH3 OR GPD3 OR YGR192C OR G7576.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 RX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=80027306; PubMed=385592;
 RA Holland J.P., Holland M.J.;
 RT "The primary structure of a glyceraldehyde-3-phosphate dehydrogenase
 gene from Saccharomyces cerevisiae.";
 RL J. Biol. Chem. 254:9839-9845(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez M.,
 Nombela C.;
 RT "The complete sequence of a 9037 bp DNA fragment of the right arm of
 Saccharomyces cerevisiae chromosome VII.";
 RL Yeast 11:587-591(1995).
 RN [3]
 RP SEQUENCE OF 46-57.
 RC STRAIN=S288C;
 RA MEDLINE=95203288; PubMed=7895733;
 RX Norbeck J., Blomberg A.;
 RT "Gene linkage of two-dimensional polyacrylamide gel electrophoresis
 resolved proteins from isogene families in Saccharomyces cerevisiae
 by microsequencing of in-gel trypsin generated peptides.";
 RL Electrophoresis 16:149-156(1995).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 NAD(+) -> 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE THREE GENES FOR GAPDH IN YEAST.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 DEHYDROGENASE FAMILY.
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 CC -----
 DR EMBL: V01300; CAA24607.1; -
 DR EMBL: J01324; AA88714.1; -
 DR EMBL: X82408; CA57803.1; -
 DR EMBL: 272977; CA97218.1; -
 DR PIR: A00371; DEBYG2.
 DR HSSP: P06977; IGAD.
 DR SWISS-2DPAGE: P00359; YEAST.
 DR COMPUTEFAST-2DPAGE: P00359; -.
 DR SGD: S0003424; TDH3.
 DR InterPro: IPR000173; GAP_dhhdhogenase.
 DR Pfam: PF00044; gpdh.1.
 DR PRINTS: PR00078; G3PDHRCNASE.
 DR PROSITE: PS00071; GAPDH.1.
 KW Glycolysis; Oxidoreductase; NAD; Multigene family.

FT INT_MET 0 0
 FT BINDING 149 149
 FT ACT_SITE 176 176
 FT CONFLICT 135 135
 FT CONFLICT 247 247
 FT CONFLICT 328 328
 SQ SEQUENCE 331 AA; 35615 MW; CFPE94A335C648B5 CRC64;
 Query Match 71.0%; Score 22; DB 1; Length 331;
 Best Local Similarity 50.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXQEND 10
 Db 69 KKIATYQEND 78
 RESULT 11
 DRK3_CHICK STANDARD; PRT; 350 AA.
 AC 090839;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (Lens fiber
 protein CLFEST4).
 GN DRK3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE= lens fibers;
 RX MEDLINE=96437509; PubMed=8840185;
 RA Sawada K., Agata K., Eguchi G.;
 RT "Characterization of terminally differentiated cell state by
 categorizing cDNA clones derived from chicken lens fibers.";
 RL Int. J. Dev. Biol. 40:531-535(1996).
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EYE LENS.
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
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 CC -----
 DR EMBL: D26311; BAA05373.1; -
 DR HSSP: P25687; IIMT.
 KW Developmental protein; Signal; Glycoprotein.
 FT SIGNAL 1 29
 FT CHAIN 1 350
 FT DOMAIN 139 187
 FT DOMAIN 200 277
 FT CARBOHYD 88 88
 FT CARBOHYD 98 98
 FT CARBOHYD 113 113
 FT CARBOHYD 196 196
 FT CARBOHYD 282 282
 SQ SEQUENCE 350 AA; 39208 MW; 57BE7ED850089DAE CRC64;
 Query Match 71.0%; Score 22; DB 1; Length 350;
 Best Local Similarity 50.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KXXXTXQEND 10
 I I I I I

Db 99 KTVOTHOEID 108

RESULT 12

YDGC_SCHPO STANDARD; PRT; 356 AA.

ID YDGC_SCHPO

AC 010498: 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C26F1.12c in chromosome I.

GN SPAC26F1.12c

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.

OX NCBI_TaxID=4896;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,

RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehmach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wandut R., Puntelle B.,

RA Goffeau A., Cadiou E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;

RT "The genome sequence of *Schizosaccharomyces pombe*."

RL Nature 415:871-880(2002).

CC -1 SIMILARITY: TO YEAST HGHL.

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CC -----

CC EMBL: 273100; CAA97369.1; -

DR Hypothetical protein.

KW

SEQUENCE 356 AA; 41260 MW; ADIBC714C134AA1C CRC64;

SO

Query Match 71.0%; Score 22; DB 1; Length 356;

Best Local Similarity 50.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10

DB 178 KYRTTLQEXD 187

RESULT 13

YB55_RICPR STANDARD; PRT; 520 AA.

ID YB55_RICPR

AC 09ZCA5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein RP855.

GN RP855.

OS Rickettsia prowazekii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI_TaxID=782;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Madrid E;

RX MEDLINE=99039499; PubMed=9823893;

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,

RA Sickeritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naslund A.K.,

RA Eriksson A.-S., Winkler H.H., Kurland C.G.;

RT "The genome sequence of *Rickettsia prowazekii* and the origin of

RT mitochondria."

RL Nature 396:133-140(1998).

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CC -----

CC EMBL: AJ235273; CAA15279.1; -

DR Hypothetical protein; Transmembrane, Complete proteome.

KW TRANSMEM 337

SEQUENCE 520 AA; 61113 MW; AAB4DBA1EE594034 CRC64;

SO

Query Match 71.0%; Score 22; DB 1; Length 520;

Best Local Similarity 50.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10

DB 374 KYRTTLQEXD 383

RESULT 14

ARS2_CAEEL STANDARD; PRT; 712 AA.

ID ARS2_CAEEL

AC 0966L5;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Arsenite-resistance protein 2 homolog.

GN E01A2.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pseudocercariae; Caenorhabditis.

OX NCBI_TaxID=6239;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;

RA Wilson R., Bentley D., Scheet P.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

CC -1 SIMILARITY: BELONGS TO THE ARS2 FAMILY.

CC -----

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CC -----

CC EMBL: AC006627; AAK85459.1; -

DR WormPep; E01A2.2; CE20643.

KW Hypothetical protein.
SQ SEQUENCE 712 AA; 80794 MW; 54B051ADFA547DE CRC64;

Query Match 71.0%; Score 22; DB 1; Length 712;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXXXXQEXD 10
| | | | |
Db 88 KKFLLTSQEDD 97

RESULT 15
YE86_SCHPO STANDARD; PRT; 886 AA.

ID YE86_SCHPO STANDARD; PRT; 886 AA.
AC 014302;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C9G1.06c in chromosome I.
GN SPAC9G1.06c.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby I., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolckele G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revelante J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT The genome sequence of Schizosaccharomyces pombe.*;
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -1- SIMILARITY: TO YEAST YDL117W.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z98763; CAB11490.1; -
CC HSSP: P29355; ISEM.
CC InterPro: IPR001452; SH3.
CC InterPro: IPR002931; Trnsglucanase_like.
CC Pfam: PF000018; SH3; 1.
CC ProDom: PD000066; SH3; 1.

DR SMART: SM00326; SH3; 1.
DR SMART: SM00460; TGC; 1.
DR PROSITE: PS50002; SH3; 1.
KW Hypothetical protein: SH3 domain.
FT DOMAIN 6 67
FT SH3.
FT POLY-SER.
SQ SEQUENCE 886 AA; 98262 MW; D0C4879C1882E869 CRC64;

Query Match 71.0%; Score 22; DB 1; Length 886;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXXXXQEXD 10
| | | | |
Db 220 KSTTSKEMD 229

Search completed: June 5, 2003, 15:56:31
Job time: 8.51515 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw'model

Run on: June 5, 2003, 15:32:58 ; Search time 29.0909 Seconds
(without alignments)
70.829 Million cell updates/sec

Title: US-09-150-947f-13

Perfect score: 31

Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirs:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	77.4	209	2	09R005
2	24	77.4	209	2	09LAE1
3	24	77.4	209	2	09LAE0
4	24	77.4	209	2	09LAD9
5	24	77.4	209	2	09LAD8
6	24	77.4	209	2	09LAD7
7	24	77.4	209	2	09LAD6
8	24	77.4	209	2	09LAD5
9	24	77.4	209	2	09LAD4
10	24	77.4	209	2	09LAD3
11	24	77.4	209	2	09LAD2
12	24	77.4	209	2	09LAD1
13	24	77.4	209	2	09LAD0
14	24	77.4	209	2	09LAC9
15	24	77.4	209	2	09LAC8
16	24	77.4	209	2	09LAC7

17	24	77.4	209	2	09LAC6	09LAC6 streptococ
18	24	77.4	209	2	09LAC5	09LAC5 streptococ
19	24	77.4	209	2	09LAC4	09LAC4 streptococ
20	24	77.4	209	2	09LAC3	09LAC3 streptococ
21	24	77.4	233	16	099XW1	099XW1 streptococ
22	24	77.4	256	2	09XSR8	09XSR8 streptococ
23	24	77.4	256	2	09S1H9	09S1H9 streptococ
24	24	77.4	256	2	09S1H8	09S1H8 streptococ
25	24	77.4	549	10	09LND29	09LND29 arabidopsi
26	24	77.4	603	12	084742	084742 human para
27	24	77.4	603	12	081076	081076 human para
28	24	77.4	955	11	090R37	090R37 mus muscu
29	24	77.4	955	11	08VHL8	08VHL8 mus muscu
30	23	74.2	234	2	09R5X4	09R5X4 staphylococ
31	23	74.2	239	2	053678	053678 staphylococ
32	23	74.2	239	2	005157	005157 staphylococ
33	23	74.2	239	2	006531	006531 staphylococ
34	23	74.2	239	2	006532	006532 staphylococ
35	23	74.2	239	2	006533	006533 staphylococ
36	23	74.2	239	2	006534	006534 staphylococ
37	23	74.2	239	2	006535	006535 staphylococ
38	23	74.2	271	2	09F0L6	09F0L6 staphylococ
39	23	74.2	324	4	043370	043370 homo sapien
40	23	74.2	405	2	09XBU4	09XBU4 bacillus ce
41	23	74.2	405	2	08VW49	08VW49 bacillus th
42	23	74.2	561	2	09X4E1	09X4E1 rhodobacter
43	23	74.2	565	16	09A2H4	09A2H4 caulobacter
44	23	74.2	565	16	098C33	098C33 rhizobium l
45	23	74.2	572	16	080818	080818 agrobacteri

ALIGNMENTS

RESULT 1

ID	PRELIMINARY:	PRT:	209 AA.
AC 09R005	01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)			
DE Mitogenic exotoxin Z 2 (Fragment).			
GN SMEZ-2.			
OS Streptococcus pyogenes.			
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;			
OC Streptococcaceae; Streptococcus.			
OX NCBI_TaxID=1314;			
RN [1]	SEQUENCE FROM N.A.		
RP STRAIN=2035;			
RC MEDLINE=99093428; PubMed=9874566;			
RX Prof. T., Mofatt S.L., Berkehn C.J., Fraser J.D.;			
RA "Identification and characterization of novel superantigens from			
RT Streptococcus pyogenes."			
RL J. Exp. Med. 189:89-102(1999).			
DR EMBL: AF086626; AAD52087.1; -.			
DR HSSP: P13163; ISXT.			
DR InterPro: IPR001961; Staph/Strep toxin.			
DR Pfam: PF01123; Staph_strep_toxin_1.			
DR PRINTS: PR002876; Staph_strep_toxin.			
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.			
FT NON_TER			
SO SEQUENCE	209 AA; 24131 MW; 52BF7911BB100152 CRC64;		

Query Match 77.4%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 125 KTVTAQED 134

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RESULT 2
Q9LAE1      PRELIMINARY;      PRT;      209 AA.
AC Q9LAE1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-3 (Fragment).
GN SMEZ-3.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11681;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24071 MW; FDADFCDD1AA87271 CRC64;

Query Match
Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
Matches 5; Conservative 50.0%; Pred. No. 46;
Matches 5; Mismatches 0; Indels 5; Gaps 0;

QY 1 KXXXTXQEXD 10
Db 125 KTYVTAQED 134

RESULT 3
Q9LAE0      PRELIMINARY;      PRT;      209 AA.
AC Q9LAE0:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-4 (Fragment).
GN SMEZ-4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9893;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24108 MW; 67EC279BBC4A8247 CRC64;

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Query Match
Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
Matches 5; Conservative 50.0%; Pred. No. 46;
Matches 5; Mismatches 0; Indels 5; Gaps 0;

QY 1 KXXXTXQEXD 10
Db 125 KTYVTAQED 134

RESULT 4
Q9LAD9      PRELIMINARY;      PRT;      209 AA.
AC Q9LAD9:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-5 (Fragment).
GN SMEZ-5.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11244;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24079 MW; 24CA3885469CBB9B CRC64;

Query Match
Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
Matches 5; Conservative 50.0%; Pred. No. 46;
Matches 5; Mismatches 0; Indels 5; Gaps 0;

QY 1 KXXXTXQEXD 10
Db 125 KTYVTAQED 134

RESULT 5
Q9LAD8      PRELIMINARY;      PRT;      209 AA.
AC Q9LAD8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-7 (Fragment).
GN SMEZ-7.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11574;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).

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DR EMBL: AF143657; AAF66657.1; -.
 DR HSSP; P13163; 1SXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_stp_toxin_1.
 DR Pfam: PF02876; Staph_stp_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24064 MW; 67B977CD5AA934F7 CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 | | | |
 DB 125 KTTVTAQED 134

RESULT 6

ID 09LAD7 PRELIMINARY; PRT; 209 AA.
 AC 09LAD7:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Mitogenic exotoxin Z-8 (Fragment).
 GN SMEZ-8.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1/5045;
 RX MEDLINE-20273982; PubMed-10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Frazer J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143658; AAF66658.1; -.
 DR HSSP; P13163; 1SXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_stp_toxin_1.
 DR Pfam: PF02876; Staph_stp_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24091 MW; 7680E9B35513DF28 CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 | | | |
 DB 125 KTTVTAQED 134

RESULT 7

ID 09LAD6 PRELIMINARY; PRT; 209 AA.
 AC 09LAD6:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Mitogenic exotoxin Z-9 (Fragment).
 GN SMEZ-9.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11299;
 RX MEDLINE-20273982; PubMed-10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Frazer J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143659; AAF66659.1; -.
 DR HSSP; P13163; 1SXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_stp_toxin_1.
 DR Pfam: PF02876; Staph_stp_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24213 MW; B21587BA33B5DD5 CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 | | | |
 DB 125 KTTVTAQED 134

RESULT 8

ID 09LAD5 PRELIMINARY; PRT; 209 AA.
 AC 09LAD5:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-10 (Fragment).
 GN SMEZ-10.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11580;
 RX MEDLINE-20273982; PubMed-10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Frazer J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143660; AAF66660.1; -.
 DR HSSP; P13163; 1SXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_stp_toxin_1.
 DR Pfam: PF02876; Staph_stp_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24102 MW; 8B4C853751A56D06 CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 | | | |
 DB 125 KTTVTAQED 134

RESULT 9

ID 09LAD4 PRELIMINARY; PRT; 209 AA.
 AC 09LAD4:

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DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9779;
RX MEDLINE-20273982; PubMed-10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Strep/Strep_toxin.
DR Pfam; PF01123; Strep_strep_toxin; 1.
DR PRINTS; PR00279; Strep_strep_toxin_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B38BD95DE CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 125 KTTVTAQED 134

RESULT 10
Q9LAD3 PRELIMINARY; PRT; 209 AA.
AC Q9LAD3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Mitogenic exotoxin Z-12 (Fragment).
GN SMEZ-12.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-10303;
RX MEDLINE-20273982; PubMed-10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143662; AAF66662.1; -.
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Strep/Strep_toxin.
DR Pfam; PF01123; Strep_strep_toxin; 1.
DR PRINTS; PR00279; Strep_strep_toxin_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24086 MW; 1C4343235157DB68 CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 KXXXTXQEXD 10
DB 125 KTTVTAQED 134

RESULT 11
Q9LAD2 PRELIMINARY; PRT; 209 AA.
AC Q9LAD2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Mitogenic exotoxin Z-13 (Fragment).
GN SMEZ-13.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95/31;
RX MEDLINE-20273982; PubMed-10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Strep/Strep_toxin.
DR Pfam; PF01123; Strep_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24072 MW; 984C1B4614589A1E CRC64;

Query Match 77.4%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 125 KTTVTAQED 134

RESULT 12
Q9LAD1 PRELIMINARY; PRT; 209 AA.
AC Q9LAD1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Mitogenic exotoxin Z-14 (Fragment).
GN SMEZ-14.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-4202;
RX MEDLINE-20273982; PubMed-10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143664; AAF66664.1; -.
DR HSSP; P13163; 1SXT.
DR InterPro; IPR001961; Strep/Strep_toxin.
DR Pfam; PF01123; Strep_strep_toxin; 1.

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DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24122 MW; 0CF5DA29E1B96EFE CRC64;

Query Match
 Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 125 KTTVTQAQED 134

RESULT 13
 ID 09LAD0 PRELIMINARY; PRT; 209 AA.

AC 09LAD0: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-15 (Fragment).
 GN SMEZ-15.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_Taxid=1314;

RP SEQUENCE FROM N.A.

RC STRAIN=;

RA MEDLINE-20273982; PubMed-10811869;

RT Profitt T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;

RT Mosaic Structure, and Significant Antigenic Variation.";
 RT J. Exp. Med. 191:1765-1776(2000).

RL EMBL; AF143665; AAF66665.1; -.

DR HSSP; P13163; ISXT.
 DR InterPro; IPR001961; Staph/Strep_toxin.

DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_toxin_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER 1
 SQ SEQUENCE 209 AA; 24209 MW; B909784ABCD1474 CRC64;

Query Match
 Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 125 KTTVTQAQED 134

RESULT 14
 ID 09LAC9 PRELIMINARY; PRT; 209 AA.

AC 09LAC9: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-16 (Fragment).
 GN SMEZ-16.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_Taxid=1314;

RP SEQUENCE FROM N.A.

RC STRAIN=10649;

RX MEDLINE-20273982; PubMed-10811869;
 RA Profitt T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,

RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143666; AAF66666.1; -.

DR HSSP; P13163; ISXT.
 DR InterPro; IPR001961; Staph/Strep_toxin.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_toxin_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER 1
 SQ SEQUENCE 209 AA; 24172 MW; A1DB8FA187098BA5 CRC64;

Query Match
 Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 125 KTTVTQAQED 134

RESULT 15
 ID 09LAC8 PRELIMINARY; PRT; 209 AA.

AC 09LAC8: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-17 (Fragment).
 GN SMEZ-17.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_Taxid=1314;

RP SEQUENCE FROM N.A.

RC STRAIN=11686;

RA MEDLINE-20273982; PubMed-10811869;

RT Profitt T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;

RT Mosaic Structure, and Significant Antigenic Variation.";
 RT J. Exp. Med. 191:1765-1776(2000).

RL EMBL; AF143667; AAF66667.1; -.

DR HSSP; P13163; ISXT.
 DR InterPro; IPR001961; Staph/Strep_toxin.

DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_toxin_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER 1
 SQ SEQUENCE 209 AA; 24181 MW; A333F46398D9DC2 CRC64;

Query Match
 Best Local Similarity 77.4%; Score 24; DB 2; Length 209;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
 DB 125 KTTVTQAQED 134

Search completed: June 5, 2003, 15:55:40
 Job time : 31.0909 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:47:43 ; Search time 33.9394 seconds
(without alignments)
39,261 Million cell updates/sec

Title: US-09-150-947F-14

Perfect score: 26

Sequence: 1 KKKXXXXXLD 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	73.1	378	21	Arabidopsis thaliana
2	18	69.2	46	21	Gene 3 human secre
3	18	69.2	46	21	Human secreted pro
4	18	69.2	147	21	Human secreted pro
5	18	69.2	152	19	Rat ninjurin 1. R
6	18	69.2	173	22	Human ninjurin 1.
7	18	69.2	173	22	Novel human diagno
8	18	69.2	200	19	Human secreted pro
9	18	69.2	213	22	Plant D-like cyclin
10	18	69.2	247	13	PCPD ORF 6. Chlam

11	18	69.2	284	23	ABP41256
12	18	69.2	406	17	AAW93144
13	18	69.2	420	17	AAW93155
14	18	69.2	420	17	AAW93157
15	18	69.2	618	22	ABG19070
16	18	69.2	705	17	AAW06831
17	18	69.2	765	22	AAW73637
18	18	69.2	765	22	AAW94373
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24	17	65.4	24	22	AAV72200
25	17	65.4	24	22	AAV72203
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27	17	65.4	76	22	ABG15641
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30	17	65.4	100	21	ABP32693
31	17	65.4	106	23	ABP32548
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33	17	65.4	142	20	AAV28349
34	17	65.4	142	21	AAW01389
35	17	65.4	142	21	AAV39026
36	17	65.4	142	22	ABW55735
37	17	65.4	143	22	ABW12218
38	17	65.4	150	20	AAV36961
39	17	65.4	153	21	AAW60296
40	17	65.4	170	23	AAW90300
41	17	65.4	171	21	AAW35162
42	17	65.4	184	22	ABW66316
43	17	65.4	186	21	AAW42925
44	17	65.4	188	21	AAW60286
45	17	65.4	189	21	AAW60295

ALIGNMENTS

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ID	AAW35560 standard; Protein; 378 AA.
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AC	AAW35560;
XX	
DT	18-OCT-2000 (first entry)
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 43459.
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KW	Protein identification: signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
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PR	19-APR-1999; 99US-0130077.

Human ovarian anti
S. lividans xylana
Streptomyces livid
Streptomyces livid
Novel human diagno
Major neutralising
Human ATP-dependen
Human protein sequ
Human ORF ORF2212
Staphylococcus aur
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Staphylococcus aur
Peptide from regio
Human ORF protein
Novel human diagno
Human polypeptide
Zea mays protein f
Zea mays protein f
Human synthase-lik
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Human secreted pro
Human secreted pro
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Human polypeptide
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Human polypeptide
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Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana

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Query Match 73.1%; Score 19; DB 21; Length 378;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
DB 13 KKAADAAALD 22

RESULT 2
AAB38172
ID AAB38172 standard; Protein; 46 AA.
XX
AC AAB38172;
XX
DT 30-JAN-2001 (first entry)
XX

DE Gene 3 human secreted protein homologous amino acid sequence #111.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
XX hyperproliferative disorder; cardiovascular disorder; angiogenesis;
XX cerebrovascular disorder; nervous system disorder; ocular disorder;
XX wound healing; skin aging; food additive; preservative.

XX Homo sapiens.

XX WO200058468-A2.

XX 05-OCT-2000.

XX 22-MAR-2000; 2000MO-US07526.

XX 26-MAR-1999; 99US-0126600.

XX 22-DEC-1999; 99US-0171550.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-611713/58.

XX Nucleic acids encoding human secreted proteins, used to prevent, treat,
XX ameliorate, or diagnose conditions such as autoimmune disorders, skin
XX disorders and cancer -

XX Disclosure; Page 362; 374pp; English.

XX The polynucleotide sequences given in AAC69399 to AAC69445 encode the
CC human secreted proteins given in AAB38119 to AAB38165. AAB38166 to
CC AAB38201 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
CC neuroprotective; antibacterial; virucide; fungicide; and
CC ophthalmological. The polynucleotides and polypeptides can be are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases, hyperproliferative disorders, cardiovascular
CC disorders, cerebrovascular disorders, angiogenesis, nervous system
CC disorders, infections caused by bacteria, viruses and fungi and ocular
CC disorders. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. AAC69390 to AAC69398 and
CC AAB38118 represent sequences used in the exemplification of the present
CC invention.

SO Sequence 46 AA;

Query Match 69.2%; Score 18; DB 21; Length 46;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
DB 19 KKSAAESMD 28

RESULT 3
AAB38173
ID AAB38173 standard; Protein; 46 AA.
XX
AC AAB38173;
XX

DT 30-JAN-2001 (first entry)
XX

DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:112.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
XX hyperproliferative disorder; cardiovascular disorder; angiogenesis;
XX cerebrovascular disorder; nervous system disorder; ocular disorder;
XX wound healing; skin aging; food additive; preservative.

XX Homo sapiens.

XX WO200058468-A2.

XX 05-OCT-2000.

XX 22-MAR-2000; 2000MO-US07526.

XX 26-MAR-1999; 99US-0126600.

XX 22-DEC-1999; 99US-0171550.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-611713/58.

XX

PT Nucleic acids encoding human secreted proteins, used to prevent, treat, ameliorate, or diagnose conditions such as autoimmune disorders, skin disorders and cancer -

PS Disclosure: Page 362; 374pp; English.

CC The polynucleotide sequences given in AAC69399 to AAC69445 encode the human secreted proteins given in AAB38119 to AAB38165. AAB38166 to AAB38201 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: immunosuppressive; antitumor; antineoplastic; antiproliferative; cytoprotective; cardioprotective; cerebroprotective; neuroprotective; ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenesis, nervous system disorders. Infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative and increase or decrease storage capabilities. AAC69390 to AAC69398 and AAC38118 represent sequences used in the exemplification of the present invention.

SO Sequence 46 AA;

Query Match 69.2%; Score 18; DB 21; Length 46;

Best Local Similarity 40.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
||
||
Db 19 KKSAAESMLD 28

RESULT 4

AAG02207 ID AAG02207 standard; Protein: 147 AA.

AC AAG02207;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 6288.

KW Human; 5' EST: expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

OS Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PS (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI: 2000-500381/45.

DR N-PSDB: AAC02213.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -

PS Claim 13; SEQ ID 6288; 71pp + CD-ROM; English.

CC The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

SO Sequence 147 AA;

Query Match 69.2%; Score 18; DB 21; Length 147;

Best Local Similarity 40.0%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
||
||
Db 78 KKKRAATTD 87

RESULT 5

AAM48271 ID AAM48271 standard; Protein: 152 AA.

AC AAM48271;

DT 23-JUN-1998 (first entry)

DE Rat. ninjurin 1.

KW Rat; ninjurin; cellular adhesion molecule; membrane bound; tumour; nerve injury induced gene; inflammation; nervous system.

OS Rattus sp.

PN WO9803650-A1.

PD 29-JAN-1998.

PF 24-JUL-1997; 97WO-US12210.

PR 24-JUL-1996; 96US-0672850.

PS (UNIT) UNIT WASHINGTON.

PI Araki T, Mibrandt J;

DR WPI: 1998-120775/11.

DR N-PSDB: AAV20665.

PT New isolated nerve injury induced (ninjurin) gene - used to develop products for treating conditions involving excessive or insufficient cellular adhesion, e.g. inflammation or tumours

PS Claim 5; Fig 1B; 80pp; English.

CC The present sequence represents rat ninjurin 1 (nerve injury induced). The ninjurin protein (NP) plays a role in axonal regeneration of peripheral nervous system (PNS) neuronal cells after injury. The products can be used for developing products for treating ninjurin mediated disorders including conditions involving inappropriate (i.e. excessive or insufficient) cellular adhesion. Conditions involving

CC excessive cellular adhesion which may be treated include e.g.
 CC inflammatory diseases such as rheumatoid arthritis, asthma, allergy
 CC conditions, adult respiratory distress syndrome, inflammatory bowel
 CC diseases (e.g. Crohn's disease, ulcerative colitis and regional
 CC enteritis) and ophthalmic inflammatory diseases, autoimmune diseases,
 CC thrombosis or inappropriate platelet aggregation conditions,
 CC arteriosclerosis, reocclusion following thrombolysis, cardiovascular
 CC diseases, some forms of diabetes and neoplastic disease including
 CC metastasis conditions. The products can also be used to promote
 CC cellular adhesion, e.g. in nerve regeneration, wound healing or
 CC prosthetic implantation. The products can also be used for detection,
 CC purification, diagnosis and screening assays.

CC Sequence 152 AA;

Query Match Best Local Similarity 69.2%; Score 18; DB 19; Length 152;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 44 KKSAAESMD 53

RESULT 6
 AAW48272
 ID AAW48272 standard; Protein: 152 AA.

AAW48272;

23-JUN-1998 (first entry)

Human nlnjurn 1.

Human; nlnjurn; cellular adhesion molecule; membrane bound; tumour;
 nerve injury induced gene; inflammation; nervous system.

Homo sapiens.

WO9803650-A1.

29-JAN-1998.

24-JUL-1997; 97WO-US12210.

24-JUL-1996; 96US-0672850.

(UNITW) UNITV WASHINGTON.

Araki T, Mlbrandt J;

WPI: 1998-120775/11.

N-PSDB; AAV20666.

New isolated nerve injury induced (nlnjurn) gene - used to develop
 products for treating conditions involving excessive or insufficient
 cellular adhesion, e.g. inflammation or tumours

Claim 6; Fig 2B; 80pp; English.

The present sequence represents human nlnjurn 1 (nerve injury induced).
 The nlnjurn protein (NP) plays a role in axonal regeneration of
 peripheral nervous system (PNS) neuronal cells after injury. The
 products can be used for developing products for treating nlnjurn
 mediated disorders including conditions involving inappropriate (i.e.
 excessive or insufficient) cellular adhesion. Conditions involving
 excessive cellular adhesion which may be treated include e.g.
 inflammatory diseases such as rheumatoid arthritis, asthma, allergy
 conditions, adult respiratory distress syndrome, inflammatory bowel
 diseases (e.g. Crohn's disease, ulcerative colitis and regional
 enteritis) and ophthalmic inflammatory diseases, autoimmune diseases,
 thrombosis or inappropriate platelet aggregation conditions,
 arteriosclerosis, reocclusion following thrombolysis, cardiovascular

CC diseases, some forms of diabetes and neoplastic disease including
 CC metastasis conditions. The products can also be used to promote
 CC cellular adhesion, e.g. in nerve regeneration, wound healing or
 CC prosthetic implantation. The products can also be used for detection,
 CC purification, diagnosis and screening assays.

CC Sequence 152 AA;

Query Match Best Local Similarity 69.2%; Score 18; DB 19; Length 152;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 44 KKSAAESMD 53

RESULT 7
 ABG20269
 ID ABG20269 standard; Protein: 173 AA.

ABG20269;

18-FEB-2002 (first entry)

Novel human diagnostic protein #20260.

Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;

WPI: 2001-639362/73.

N-PSDB; AAS84456.

New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity

Claim 20; SEQ ID NO 50628; 103pp; English.

The invention relates to isolated polynucleotide (I) and
 polypeptide (II) sequences. (I) is useful as hybridisation probes,
 polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 and gene mapping, and in recombinant production of (II). The
 polynucleotides are also used in diagnostics as expressed sequence tags
 for identifying expressed genes. (I) is useful in gene therapy techniques
 to restore normal activity of (II) or to treat disease states involving
 (II). (II) is useful for generating antibodies against it, detecting or
 quantitating a polypeptide in tissue, as molecular weight markers and as
 a food supplement. (II) and its binding partners are useful in medical
 imaging of sites expressing (II). (I) and (II) are useful for treating
 disorders involving aberrant protein expression or biological activity.
 The polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 amino acid sequences. ABG00010-ABG30377 represent novel human
 diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 173 AA;

Query Match 69.2%; Score 18; DB 22; Length 173;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 141 KKAASHRALD 150

RESULT 8
AAW74903
ID AAW74903 standard; Protein; 200 AA.

AC AAW74903;

DT 25-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 176 clone HPTBR48.

XX Human; secreted protein; testis; tumour; foetal brain tissue;
XX Fusion protein; cancer; central nervous system; seizure;
XX diagnosis; neurodegenerative disease.

OS Homo sapiens.

EH Key Location/Qualifiers
FT Misc-difference 200
XX /label- unknown

PN WO9839448-A2.

XX 11-SEP-1998.

PF 06-MAR-1998; 98WO-US04493.

PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040335.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.

PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047616.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056330.
PR 22-AUG-1997; 97US-0056331.
PR 22-AUG-1997; 97US-0056332.
PR 22-AUG-1997; 97US-0056336.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056896.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.

(HUMA-) HUMAN GENOME SCI INC.
PA Bednarik DP, Brewer LA, Carter KC, Duan R, Ehner R, Endress GA,
XX Feng P, Fertie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
PI Kyaw H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,

PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI; 1998-506364/43.
DR N-PSDB; AAV59686.
XX
PT New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 649-650, 721pp; English.
XX
CC This sequence represents a secreted human protein encoded by the nucleic
CC acid molecule designated Gene 176 from the human CDNA clone HPTBR48
CC (deposited as clone ATCC 97904 and ATCC 209050).
CC The gene can be used to generate fusion proteins by linking to the gene
CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW4731-W5026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).
XX
SQ Sequence 200 AA;
XX
Query Match 69.2%; Score 18; DB 19; Length 200;
Best Local Similarity 40.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 KKKXXXXXLD 10
|| ||
DB 151 KKAASHRAD 160
XX
RESULT 9
AAB47003
ID AAB47003 standard; Protein; 213 AA.
XX
AC AAB47003;
XX
DE 22-MAR-2001 (first entry)
XX
XX Plant D-like cyclin inhibitor BRO2.
XX
XX Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
XX growth rate; dividing cells; inactivation; protoplast; seed;
XX root cell; meristem; leaf.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX Protein 20..147
XX /Label= BRO2
XX
XX WO200069883-A1.
XX
XX 23-NOV-2000.
XX
XX 15-MAY-2000; 2000WO-US13379.
XX
XX 14-MAY-1999; 99US-0134373.
XX
XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
XX Roberts J, Kelly B;
XX
XX WPI; 2001-024998/03.
XX
XX N-PSDB; AAC85203.
XX

PT Functionally inactivating expression of plant D-like cyclin inhibitor
PT gene for producing a hyperplastic variant plant, modulating the growth
PT and/or yield of plants, and increasing the proportion of dividing cells
XX
XX Example 1; Page 38-39, 50pp; English.
PS
XX
CC The sequence given in AAB47003 represents a plant D1 cyclin
CC inhibitor, BRO2. The DNA encoding this sequence was isolated using
CC a yeast two hybrid screen. The BRO2 protein was found to contain a
CC seven amino acid sequence cyclin binding domain similar to that of
CC BRO1, BRO3 and BRO4 (see also AAB47005-6). The DNA encoding this
CC sequence is homologous to a sequence present in a D-like cyclin
CC inhibitor gene and when integrated at the corresponding locus,
CC functionally inactivates plant D-like cyclin inhibitor protein
CC expression. The BRO4 coding sequence may be used to produce a
CC hyperplastic variant plant, increase the growth rate of a plant,
CC or increase the proportion of dividing cells in a plant cell
CC population, relative to a wild-type plant, by functionally
CC inactivating the expression of a plant D-like cyclin inhibitor
CC gene in a plant. BRO4 is useful for increasing the proportion of
CC dividing cells in a plant cell population comprising protoplast,
CC seeds, root cells, meristem cells or leaf cells.
XX
SQ Sequence 213 AA;
XX
Query Match 69.2%; Score 18; DB 22; Length 213;
Best Local Similarity 40.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 KKKXXXXXLD 10
|| ||
DB 10 KKTFTYTSLD 19
XX
RESULT 10
AAR29641
ID AAR29641 standard; Protein; 247 AA.
XX
AC AAR29641;
XX
DE 05-FEB-1993 (first entry)
XX
XX PCTD ORF 6.
XX
XX CT; PCTD; epithelium; ocula mucosa; uro-genital mucosa; antigen;
XX monoclonal; polyclonal; antibody; vaccine.
XX
XX Chlamydia trachomatis.
XX
XX OS
XX Chlamydia trachomatis.
XX
XX EP499681-A.
XX
XX 26-AUG-1992.
XX
XX 17-APR-1991; 91EP-0106110.
XX
XX 07-FEB-1991; 91IT-0000314.
XX
XX (ISTS) SCLAVO SPA.
XX
XX Comanducci M, Giuliani MM, Ratti G, Tecce MF;
XX
XX WPI; 1992-285922/35.
XX
XX N-PSDB; AAQ27429.
XX
XX PCTD plasmid from Chlamydia Trachomatis and immunogenic proteins
XX - for diagnosing and vaccinating against Chlamydia infections
XX e.g. venereal lymphogranuloma
XX
XX Claim 1; Page 8-16; 40pp; English.
XX
XX The sequences given in AAR29636-43 are encoded by the plasmid isolated
XX from Chlamydia trachomatis (CT) serotype D, PCTD. This serotype
XX generally infects epithelial tissues, such as the ocular and

uro-genital mucous membranes, and shows a low virulence. Of the eight proteins encoded by the plasmid, seven are encoded by the sense strand and the eighth is encoded by the complementary strand. These proteins can be used as antigens for the preparation of poly- and mono-clonal antibodies to be used in diagnostics. The antigens can also be used in the formulation of vaccines against infections due to CT.

Sequence 247 AA:

Query Match 69.2%; Score 18; DB 13; Length 247;
Best Local Similarity 40.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXD 10
13 KKNQTAASLD 22

RESULT 11

ABP41256 standard; Protein; 284 AA.

ABP41256;
22-AUG-2002 (first entry)

Human ovarian antigen HOFNY16, SEQ ID NO:2388.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytotoxic; immunomodulatory; neuroprotective;
antiinflammatory; gynaecological; reproductive.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US18569.

07-JUN-2000; 2000US-209467P.

(HUMA-) HUMAN GENOME SCI INC.

Blrse CE, Rosen CA;

WPI; 2002-147878/19.

N-PSDB; AB054333.

Isolated nucleic acid molecules encoding novel ovarian polypeptides,
useful in the prevention, treatment and diagnosis of cancer (e.g.
neurological diseases -

Claim 11; SEQ ID NO 2388; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
ABP43228) and to cdnas encoding them (AB054131-AB056305), and also
encompasses polypeptides 90% identical and polynucleotides 95% identical
to the sequences of the invention. The invention additionally relates to
recombinant vectors and host cells comprising human ovarian antigen
polynucleotides, antibodies against human ovarian antigens, and the use
of ovarian antigen polynucleotides and polypeptides in diagnosing,
treating, prognosing or preventing various ovary and/or breast-related
disorders. Such conditions include ovarian cancer and breast cancer, and
metastatic tumours of ovarian or breast origin, reproductive system

disorders (e.g., infertility, disorders of pregnancy, anovulation,
polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
vaginitis), immune disorders (e.g., congenital and acquired
immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
blood-related disorders (e.g., anaemia), cardiovascular disorders,
respiratory disorders, neurological disorders, gastrointestinal disorders
and urinary system disorders. Ovarian antigen polypeptides and
polynucleotides may also be used in screening for compounds which
modulate ovarian antigen expression or activity. The polynucleotides may
further be used for gene therapy, chromosome mapping, in the
identification of individuals and in forensic analysis, and the
polypeptides may be used as food additives or to prepare antibodies
useful in disease diagnosis, drug targeting and phenotyping. The present
sequence represents a human ovarian antigen of the invention.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

Sequence 284 AA:

Query Match 69.2%; Score 18; DB 23; Length 284;
Best Local Similarity 40.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXD 10
236 KKAASHRALD 245

RESULT 12

AAW93144 standard; Protein; 406 AA.

AAW93144;

21-MAY-1999 (first entry)

S. lividans xylanase A protein Stmk1a.

Xylanase A; acidophilic; thermostable; XYL I; XYL II; plant biomass;
hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin.

Streptomyces lividans.

US5871730-A.

16-FEB-1999.

29-JUL-1994; 94US-0282197.

29-JUL-1994; 94US-0282197.

(UTSH) UNITV SHERBROOKE.

Beaulieu C, Brzezinski R, Dery CV;

WPI; 1996-141348/15.

New acidophilic and thermostable xylanase enzymes from Actinomadura
sp. FC7 - useful for treating plant biomass, especially paper and
wood pulp, to degrade hemicellulose and hydrolyse xylan

Example 8; Fig 10; 60pp; English.

This invention describes the use of novel acidophilic and thermostable
xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
retain their activity under harsh industrial conditions (e.g. high
temperature or wide pH ranges) and may be secreted by recombinant host
cells, to treat plant biomass. Xylanases XYL I and XYL II are part of
a large group of hemicellulase enzymes and function by cutting the

CC . beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose
CC residues that is a major constituent of hemicellulose). This means that
CC they may be used in the paper and pulp industry to improve the efficiency
CC of the bleaching process by degrading the structure of the material.
CC XYL I and XYL II may also be used to treat feed, by degrading a
CC substrate with a high beta-glucan or cellulose content. XYL I and XYL II
CC retain their activity at high temperatures (e.g. 70 deg. C) and at low
CC pHs (e.g. 4.0), conditions which tend to denature most known xylanases.
CC Enzymes that remain active in these conditions may be used in industrial
CC processes that are carried out at high temperature and low pH to speed up
CC other, non-enzymatic reactions, minimising costs, energy requirements,
CC and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
CC bleaching agents to penetrate better, to remove lignin from the pulp and
CC 'bleach' the colouration from it. This means smaller quantities of the
CC agents can be used to produce the same or a better result. Also,
CC disrupting the structure aids water drainage.
CC NOTE: This patent is an equivalent to FI9503640.
CC
XX

SQ Sequence 406 AA;

Query Match 69.2%; Score 18; DB 17; Length 406;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 330 KKAATYAVLD 339

RESULT 13
AAW93155

ID AAW93155 standard; Protein; 420 AA.

XX AAW93155;

DT 21-MAY-1999 (first entry)

XX Streptomyces lividans xylanase A protein.

KW Xylanase A; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KM hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin.

XX Streptomyces lividans.

OS Streptomyces lividans.

PN US5871730-A.

PD 16-FEB-1999.

PF 29-JUL-1994; 94US-0282197.

PR 29-JUL-1994; 94US-0282197.

PA (UYSH) UNIV SHERBROOKE.

PI Beaulieu C., Brzezinski R., Dery CV;

DR WPI; 1996-141348/15.

PT New acidophilic and thermostable xylanase enzymes from Actinomadura

PT sp. FC7 - useful for treating plant biomass, especially paper and

PS Example 8; Fig 11; 60pp; English.

CC This invention describes the use of novel acidophilic and thermostable
CC xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
CC retain their activity under harsh industrial conditions (e.g. high
CC temperature or wide pH ranges) and may be secreted by recombinant host
CC cells, to treat plant biomass. Xylanases XYL I and XYL II are part of
CC a large group of hemicellulase enzymes and function by cutting the

CC beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose
CC residues that is a major constituent of hemicellulose). This means that
CC they may be used in the paper and pulp industry to improve the efficiency
CC of the bleaching process by degrading the structure of the material.
CC XYL I and XYL II may also be used to treat feed, by degrading a
CC substrate with a high beta-glucan or cellulose content. XYL I and XYL II
CC retain their activity at high temperatures (e.g. 70 deg. C) and at low
CC pHs (e.g. 4.0), conditions which tend to denature most known xylanases.
CC Enzymes that remain active in these conditions may be used in industrial
CC processes that are carried out at high temperature and low pH to speed up
CC other, non-enzymatic reactions, minimising costs, energy requirements,
CC and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
CC bleaching agents to penetrate better, to remove lignin from the pulp and
CC 'bleach' the colouration from it. This means smaller quantities of the
CC agents can be used to produce the same or a better result. Also,
CC disrupting the structure aids water drainage.
CC NOTE: This patent is an equivalent to FI9503640.
CC
XX

SQ Sequence 420 AA;

Query Match 69.2%; Score 18; DB 17; Length 420;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 330 KKAATYAVLD 339

RESULT 14
AAW93157

ID AAW93157 standard; Protein; 420 AA.

XX AAW93157;

DT 21-MAY-1999 (first entry)

XX Streptomyces lividans xylanase A protein.

KW Xylanase A; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KM hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin.

XX Streptomyces lividans.

OS Streptomyces lividans.

PN US5871730-A.

PD 16-FEB-1999.

PF 29-JUL-1994; 94US-0282197.

PR 29-JUL-1994; 94US-0282197.

PA (UYSH) UNIV SHERBROOKE.

PI Beaulieu C., Brzezinski R., Dery CV;

DR WPI; 1996-141348/15.

PT New acidophilic and thermostable xylanase enzymes from Actinomadura

PT sp. FC7 - useful for treating plant biomass, especially paper and

PS Example 9; Fig 13; 60pp; English.

CC This invention describes the use of novel acidophilic and thermostable
CC xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
CC retain their activity under harsh industrial conditions (e.g. high
CC temperature or wide pH ranges) and may be secreted by recombinant host
CC cells, to treat plant biomass. Xylanases XYL I and XYL II are part of
CC a large group of hemicellulase enzymes and function by cutting the

CC beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose
 CC residues that is a major constituent of hemicellulose). This means that
 CC they may be used in the paper and pulp industry to improve the efficiency
 CC of the bleaching process by degrading the structure of the material.
 CC XYL I and XYL II may also be used to treat feed, by degrading a
 CC substrate with a high beta-glucan or cellulose content. XYL I and XYL II
 CC retain their activity at high temperatures (e.g. 70 deg. C) and at low
 CC pHs (e.g. 4.0), conditions which tend to denature most known xylanases.
 CC Enzymes that remain active in these conditions may be used in industrial
 CC processes that are carried out at high temperature and low pH to speed up
 CC other, non-enzymatic reactions, minimising costs, energy requirements,
 CC and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
 CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
 CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
 CC bleaching agents to penetrate better, to remove lignin from the pulp and
 CC 'bleach' the colouration from it. This means smaller quantities of the
 CC agents can be used to produce the same or a better result. Also,
 CC disrupting the structure aids water drainage.
 CC NOTE: This patent is an equivalent to F19503640.

SQ Sequence 420 AA:

Query Match 69.2%; Score 18; DB 17; Length 420;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXD 10

DB 330 KKAAYTAVLD 339

RESULT 15

ABG19070 standard; Protein; 618 AA.

AC ABG19070;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #19061.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR MPI; 2001-639362/73.

DR N-PSDB; AAS83257.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 20: SEQ ID NO 49429; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. Abg00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 618 AA:

Query Match 69.2%; Score 18; DB 22; Length 618;

Best Local Similarity 40.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXD 10

DB 372 KKVTLSTSD 381

Search completed: June 5, 2003, 16:00:23
 JOD time : 34.9394 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:23:33 ; Search time 8.78788 Seconds
(Without alignments)
33.481 Million cell updates/sec

Title: US-09-150-947F-14
Perfect score: 26
Sequence: 1 KXXXXXXXXXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCOTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	100	4	US-08-672-850-13
2	18	69.2	152	4	US-08-672-850-4
3	18	69.2	152	4	US-08-672-850-6
4	18	69.2	152	4	US-08-672-850-12
5	18	69.2	200	4	US-09-149-476-495
6	18	69.2	200	4	US-08-333-750C-32
7	18	69.2	237	2	US-09-234-613-32
8	18	69.2	247	3	US-08-969-644-18
9	18	69.2	247	3	US-08-444-189-18
10	18	69.2	247	3	US-08-468-544-18
11	18	69.2	406	2	US-08-282-197C-52
12	18	69.2	420	2	US-08-282-197C-63
13	18	69.2	420	2	US-08-282-197C-66
14	18	69.2	491	2	US-08-468-812-8
15	18	69.2	491	4	US-08-590-563-8
16	18	69.2	705	2	US-08-663-566A-19
17	18	69.2	705	2	US-08-023-610-19
18	18	69.2	705	2	US-08-288-065A-19
19	18	69.2	705	2	US-08-362-240A-19
20	18	69.2	705	5	PCT-US95-10245-19
21	17	65.4	17	4	US-08-896-933-6
22	17	65.4	17	4	US-08-896-933-19
23	17	65.4	17	4	US-09-314-235-6
24	17	65.4	17	4	US-09-314-235-19
25	17	65.4	24	3	US-08-838-413A-20
26	17	65.4	24	3	US-08-838-413A-27
27	17	65.4	142	4	US-08-672-850-8

28	17	65.4	193	4	US-08-896-933-31	Sequence 31, Appl
29	17	65.4	193	4	US-09-314-235-31	Sequence 31, Appl
30	17	65.4	194	1	US-08-446-918A-6	Sequence 6, Appl1
31	17	65.4	194	2	US-08-580-806-6	Sequence 6, Appl1
32	17	65.4	224	1	US-08-152-456A-2	Sequence 2, Appl1
33	17	65.4	234	1	US-08-440-221-2	Sequence 2, Appl1
34	17	65.4	234	3	US-08-486-099-111	Sequence 11, App
35	17	65.4	234	3	US-08-360-107A-121	Sequence 121, App
36	17	65.4	234	3	US-08-484-223B-111	Sequence 111, App
37	17	65.4	234	3	US-08-919-597-111	Sequence 111, App
38	17	65.4	234	3	US-08-475-668A-111	Sequence 111, App
39	17	65.4	234	3	US-08-485-551A-111	Sequence 111, App
40	17	65.4	234	3	US-08-471-913A-111	Sequence 111, App
41	17	65.4	234	4	US-08-485-264A-111	Sequence 111, App
42	17	65.4	234	4	US-08-474-249A-111	Sequence 111, App
43	17	65.4	234	4	US-09-144-776B-12	Sequence 12, Appl
44	17	65.4	238	4	US-08-896-933-28	Sequence 28, Appl
45	17	65.4	238	4	US-09-314-235-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-672-850-13
Sequence 13, Application US/08672850
Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Mubrandt, Jeffrey
APPLICANT: Ataki, Yoshiyuki
TITLE OF INVENTION: NINURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-672-850-13

Query Match 69.2%; Score 18; DB 4; Length 100;
Best Local Similarity 40.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Ox 1 KXXXXXXXXXD 10
Db 44 KKAASMD 53

RESULT 2
US-08-672-850-4
Sequence 4, Application US/08672850
Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey
APPLICANT: Ataki, Toshiyuki
TITLE OF INVENTION: NINTURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-672-850-4

Query Match 69.2%; Score 18; DB 4; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 44 KKSAAESMLD 53

RESULT 3
US-08-672-850-6
Sequence 6, Application US/08672850
Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey
APPLICANT: Ataki, Toshiyuki
TITLE OF INVENTION: NINTURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850

FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-672-850-6

Query Match 69.2%; Score 18; DB 4; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 44 KKSAAESMLD 53

RESULT 4
US-08-672-850-12
Sequence 12, Application US/08672850
Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey
APPLICANT: Ataki, Toshiyuki
TITLE OF INVENTION: NINTURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-672-850-12

Query Match 69.2%; Score 18; DB 4; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

Fri Jun 6 09:14:32 2003

DB 44 KRSAESMLD 53

RESULT 5

US-09-149-476-495

Sequence 495, Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,163

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/047,600

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,615

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,597

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,502

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,633

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,583

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,617

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,618

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,503

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,592

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,581

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,584

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,500

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,587

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,492

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,598

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,613

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,582

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,596

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,612

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,632

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,601

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/043,580

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,568

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,314

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,569

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,311

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,671

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,674

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,669

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,312

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,313

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,672

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,315

EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/048,974

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/056,886

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,877

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,889

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,893

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,630

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,878

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,662

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,872

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,882

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,637

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,903

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,888

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,879

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,880

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,894

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,911

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,636

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,874

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,864

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,631

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,845

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,892

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 69.2%; Score 18; DB 4; Length 200;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXLD 10
11
DB 151 KKAASHRALD 160

RESULT 6
US-08-933-750C-32
Sequence 32, Application US/08933750C

Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLANDNOT03
CLONE: 1602473
US-08-933-750C-32

Query Match 69.2%; Score 18; DB 2; Length 237;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXLD 10
11
DB 189 KKAASHRALD 198

RESULT 7
US-09-234-613-32
Sequence 32, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1602473
US-09-234-613-32

Query Match 69.2%; Score 18; DB 4; Length 237;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 189 KKAASHRALD 198

RESULT 8
US-08-969-644-18
Sequence 18, Application US/08969644
Patent No. 6096519
GENERAL INFORMATION:
APPLICANT: Ratelli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCID PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-644-18

Query Match 69.2%; Score 18; DB 3; Length 247;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 13 KKNQTRASLD 22

RESULT 9
US-08-444-189-18
Sequence 18, Application US/08444189
Patent No. 6110705
GENERAL INFORMATION:
APPLICANT: Ratelli, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCID PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820

FILING DATE: IT MI 91A000314
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-189-18

Query Match 69.2%; Score 18; DB 3; Length 247;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy: 1 KXXXXXXLD 10
13 KKNQTAASLD 22

RESULT 10
US-08-468-544-18
Sequence 18, Application US/08468544
Patent No. 6248563

GENERAL INFORMATION:
APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCID PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991

ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-544-18

Query Match 69.2%; Score 18; DB 4; Length 247;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy: 1 KXXXXXXLD 10
13 KKNQTAASLD 22

RESULT 11
US-08-282-197C-52
Sequence 52, Application US/08282197C
Patent No. 5871730

GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050,0410000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-52

Query Match 69.2%; Score 18; DB 2; Length 406;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy: 1 KXXXXXXLD 10
330 KKAATYAVLD 339

RESULT 12
US-08-282-197C-63
Sequence 63, Application US/08282197C
Patent No. 5871730

GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole

TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-63

Query Match 69.2%; Score 18; DB 2; Length 420;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXD 10
DB 330 KKAATYAVLD 339

RESULT 13
US-08-282-197C-66
Sequence 66, Application US/08282197C
Patent No. 5871730
GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-66

Query Match 69.2%; Score 18; DB 2; Length 420;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXD 10
DB 330 KKAATYAVLD 339

RESULT 14
US-08-468-812-8
Sequence 8, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaanper, Jari
APPLICANT: M ntyl, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-468-812-8

Query Match
Best Local Similarity 40.0%; Score 18; DB 2; Length 491;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 333 KKAAYTAVLD 342

RESULT 15
US-08-590-563-8
Sequence 8, Application US/08590563
Patent No. 6300114

GENERAL INFORMATION:

APPLICANT: M ntyl, Arja
APPLICANT: Veinmaaier, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Plirko
APPLICANT: Lahtinen, Taria
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-590-563-8

Query Match
Best Local Similarity 40.0%; Score 18; DB 4; Length 491;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 333 KKAAYTAVLD 342

Search completed: June 5, 2003, 15:32:43
Job time: 9.78788 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:01 ; Search time 12.1212 Seconds
(without alignments)
85.173 Million cell updates/sec

Title: US-09-150-947f-14
Perfect score: 26
Sequence: 1 KRXXXXXXID 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	69.2	200	9	US-09-809-391-495
2	18	69.2	237	10	US-09-840-787-32
3	18	69.2	365	9	US-10-125-692-16
4	18	69.2	491	10	US-09-770-621-8
5	17	65.4	12	9	US-10-113-809-3
6	17	65.4	58	12	US-10-001-879-145
7	17	65.4	107	9	US-09-465-714-4
8	17	65.4	142	10	US-09-729-674-76
9	17	65.4	151	9	US-09-465-714-2
10	17	65.4	194	9	US-09-465-714-3
11	17	65.4	233	1	US-08-882-431-12
12	17	65.4	234	9	US-09-870-759-18
13	17	65.4	234	9	US-10-002-784A-12
14	17	65.4	238	9	US-09-465-714-1
15	17	65.4	266	1	US-08-882-431-14
16	17	65.4	266	9	US-09-870-759-12
17	17	65.4	266	9	US-10-002-784A-14
18	17	65.4	383	9	US-09-738-626-6821
19	17	65.4	490	10	US-09-841-132-434

20	17	65.4	582	9	US-10-046-938-29	Sequence 29, Appl
21	17	65.4	623	9	US-09-738-626-5990	Sequence 5990, Ap
22	16	61.5	10	10	US-09-150-947B-3	Sequence 3, Appl1
23	16	61.5	10	10	US-09-150-947B-4	Sequence 4, Appl1
24	16	61.5	12	9	US-10-113-809-1	Sequence 1, Appl1
25	16	61.5	12	9	US-10-113-809-4	Sequence 4, Appl1
26	16	61.5	12	10	US-09-150-947B-2	Sequence 2, Appl1
27	16	61.5	13	10	US-09-150-947B-5	Sequence 5, Appl1
28	16	61.5	13	10	US-09-150-947B-6	Sequence 6, Appl1
29	16	61.5	13	10	US-09-150-947B-11	Sequence 11, Appl
30	16	61.5	14	10	US-09-150-947B-9	Sequence 9, Appl1
31	16	61.5	14	10	US-09-150-947B-10	Sequence 10, Appl1
32	16	61.5	16	10	US-09-150-947B-7	Sequence 7, Appl1
33	16	61.5	25	10	US-09-803-165-29	Sequence 29, Appl
34	16	61.5	26	10	US-09-150-947B-8	Sequence 8, Appl1
35	16	61.5	35	10	US-09-150-947B-8	Sequence 8, Appl1
36	16	61.5	36	9	US-09-764-891-4313	Sequence 4313, Ap
37	16	61.5	38	10	US-09-071-838-150	Sequence 150, Ap
38	16	61.5	39	10	US-09-843-845-12	Sequence 12, Appl
39	16	61.5	63	9	US-10-044-692-65	Sequence 65, Appl
40	16	61.5	63	9	US-10-044-539-65	Sequence 65, Appl
41	16	61.5	69	9	US-09-843-676-16	Sequence 16, Appl
42	16	61.5	69	9	US-09-766-253-16	Sequence 16, Appl
43	16	61.5	69	9	US-09-438-486-16	Sequence 16, Appl
44	16	61.5	69	9	US-10-053-758-16	Sequence 16, Appl
45	16	61.5	69	9	US-10-054-295-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-809-391-495
; Sequence 495, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; PRIOR APPLICATION DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 495
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (200)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-495

Query Match 69.2%; Score 18; DB 9; Length 200;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KRXXXXXXID 10
DB 151 KKAASHRALD 160

RESULT 2
US-09-840-787-32
; Sequence 32, Application US/09840787
; Patent No. US20020058264A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Hillman, Jennifer L.
; Bandman, Olga
; Shah, Purvi
; Au-Young, Janice

Yue, Henry
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1602473
SEQUENCE DESCRIPTION: SEQ ID NO: 32 :
US-09-840-787-32
Query Match 69.2%; Score 18; DB 10; Length 237;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 KKKXXXXXXLD 10
DB 189 KKAASHRALD 198
RESULT 3
US-10-125-692-16
Sequence 16, Application US/10125692
Publication No. US20030044429A1
GENERAL INFORMATION:
APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka
APPLICANT: Smith, Kelly D.
APPLICANT: Underhill, David M.
TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
TITLE OF INVENTION: of use
FILE REFERENCE: P-IS 5155
CURRENT APPLICATION NUMBER: US/10/125,692
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16

LENGTH: 365
TYPE: PRT
ORGANISM: P. mirabilis1
US-10-125-692-16
Query Match 69.2%; Score 18; DB 9; Length 365;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 KKKXXXXXXLD 10
DB 197 KKNAAATLD 206
RESULT 4
US-09-770-621-8
Sequence 8, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmaaper, Jari
APPLICANT: Pagarstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirko
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-09-770-621-8

Query Match 69.2%; Score 18; DB 10; Length 491;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXD 10
DB 333 KKAAYTAVLD 342

RESULT 5

US-10-113-809-3
; Sequence 3, Application US/10113809
; Patent No. US2002017573A1
; GENERAL INFORMATION:
; APPLICANT: Maschke, Hans, E.
; TITLE OF INVENTION: EXOTOXIN-LIGAND
; FILE REFERENCE: MBP-011XX
; CURRENT APPLICATION NUMBER: US/10/113,809
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 101 16 042.9-41
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacterial Toxin Binding Ligand
US-10-113-809-3

Query Match 65.4%; Score 17; DB 9; Length 12;
Best Local Similarity 40.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXD 10
DB 3 KKLAISTLD 12

RESULT 6

US-10-001-879-145
; Sequence 145, Application US/10001879
; Patent No. US20020127237A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Caferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-145

Query Match 65.4%; Score 17; DB 12; Length 58;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXD 10
DB 3 KKLAISTLD 12

DB 42 KKRTOATLD 51

RESULT 7

US-09-465-714-4
; Sequence 4, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Truncated bacterial sequence
US-09-465-714-4

Query Match 65.4%; Score 17; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXD 10
DB 34 KKLAISTLD 43

RESULT 8

US-09-729-674-76
; Sequence 76, Application US/09729674
; Patent No. US20010039335A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Werberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steindinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; TITLE OF INVENTION: GENETICS INSTITUTE, INC.
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-674-76

Query Match 65.4%; Score 17; DB 10; Length 142;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXKD 10
 DB 30 KKSVAESMID 39

RESULT 9
 US-09-465-714-2

Sequence 2, Application US/09465714
 Publication No. US20030032582A1
 GENERAL INFORMATION:
 APPLICANT: Wahlsten, Jennifer L.
 APPLICANT: Ramakrishnan, S.
 APPLICANT: Schlievert, Patrick M.
 TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
 FILE REFERENCE: 09531/003001
 CURRENT APPLICATION NUMBER: US/09/465,714
 CURRENT FILING DATE: 1999-12-17
 PRIOR APPLICATION NUMBER: 09/001,593
 PRIOR FILING DATE: 1998-12-31
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 151
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Hybrid containing bacterial and mammalian sequence
 US-09-465-714-2

Query Match 65.4%; Score 17; DB 9; Length 151;
 Best Local Similarity 40.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXKD 10
 DB 34 KKQIAISTLD 43

RESULT 10
 US-09-465-714-3
 Sequence 3, Application US/09465714
 Publication No. US20030032582A1
 GENERAL INFORMATION:
 APPLICANT: Wahlsten, Jennifer L.
 APPLICANT: Ramakrishnan, S.
 APPLICANT: Schlievert, Patrick M.
 TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
 FILE REFERENCE: 09531/003001
 CURRENT APPLICATION NUMBER: US/09/465,714
 CURRENT FILING DATE: 1999-12-17
 PRIOR APPLICATION NUMBER: 09/001,593
 PRIOR FILING DATE: 1998-12-31
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Bacterial Sequence
 US-09-465-714-3

Query Match 65.4%; Score 17; DB 9; Length 194;
 Best Local Similarity 40.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXKD 10
 DB 121 KKQIAISTLD 130

RESULT 11
 US-08-882-431-12
 Sequence 12, Application US/08882431
 Publication No. US20030009015A1

GENERAL INFORMATION:
 APPLICANT: Robert G. Ulrich,
 APPLICANT: Mark A. Olson
 APPLICANT: Sina Bavari
 TITLE OF INVENTION: Bacterial Superantigen
 TITLE OF INVENTION: Vaccines
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John Moran
 STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
 CITY: FORT DETRICK
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/882,431
 FILING DATE: June 25, 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Moran, John
 REGISTRATION NUMBER: 26,313
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 233
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 US-08-882-431-12

Query Match 65.4%; Score 17; DB 1; Length 233;
 Best Local Similarity 40.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXKD 10
 DB 160 KKQIAISTLD 169

RESULT 12
 US-09-870-759-18
 Sequence 18, Application US/09870759
 Patent No. US20020177551A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 18
 LENGTH: 234
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-870-759-18

Query Match 65.4%; Score 17; DB 9; Length 234;
 Best Local Similarity 40.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXLD 10
||
Db 161 KKOLAISTLD 170

RESULT 13
US-10-002-784A-12
; Sequence 12, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: toxin shock syndrom toxin-1 mutant
US-10-002-784A-12

Query Match 65.4%; Score 17; DB 9; Length 234;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXLD 10
||
Db 161 KKOLAISTLD 170

RESULT 14
US-09-465-714-1
; Sequence 1, Application US/09465714
; Publication No. US2003032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid containing bacterial and mammalian sequence
US-09-465-714-1

Query Match 65.4%; Score 17; DB 9; Length 238;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXLD 10
||
Db 121 KKOLAISTLD 130

RESULT 15

US-08-882-431-14
; Sequence 14, Application US/0882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match 65.4%; Score 17; DB 1; Length 266;
Best Local Similarity 40.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXLD 10
||
Db 178 KKVTAQELD 187

Search completed: June 5, 2003, 15:49:03
Job time: 13.1212 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:24:01 ; Search time 9.84848 seconds
(without alignments)
97.613 Million cell updates/sec

Title: US-09-150-947F-14

Perfect score: 26

Sequence: 1 KXXXXXXXXXD 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	73.1	284	2	T50261 conserved hypothet
2	19	73.1	378	2	E84806 probable elongatio
3	18	69.2	100	1	R3LV14 ribosomal protein
4	18	69.2	159	2	T48837 hypothetical prote
5	18	69.2	161	2	A82401 transcription regu
6	18	69.2	169	2	S07748 hypothetical prote
7	18	69.2	171	2	A96723 hypothetical prote
8	18	69.2	212	2	C90786 probable tet opero
9	18	69.2	212	2	A85646 probable transcrip
10	18	69.2	212	2	C64843 hypothetical prote
11	18	69.2	217	2	B64080 hypothetical prote
12	18	69.2	237	2	T14770 hypothetical prote
13	18	69.2	247	2	S01924 hypothetical prote
14	18	69.2	247	2	F37386 hypothetical prote
15	18	69.2	278	2	A83091 hypothetical prote
16	18	69.2	278	2	H98195 hypothetical prote
17	18	69.2	344	2	S22796 probable portal pr
18	18	69.2	365	2	UC2559 flagellin flhC-1 -
19	18	69.2	383	2	T34603 xylanase A - Stre
20	18	69.2	413	2	S73643 MG349 homolog G12
21	18	69.2	427	2	A41790 actin like protein
22	18	69.2	477	1	US0589 endo-1,4-beta-xyla
23	18	69.2	543	2	T32496 hypothetical prote
24	18	69.2	837	2	S64785 hypothetical prote
25	18	69.2	858	2	T24062 hypothetical prote
26	18	69.2	863	2	G96964 probable permease,
27	18	69.2	1035	2	T16588 hypothetical prote
28	18	69.2	1042	2	T16169 hypothetical prote
29	18	69.2	1279	2	T17194 protoporphylin IX

30	17	65.4	109	2	A69448 hypothetical prote
31	17	65.4	118	2	T15655 hypothetical prote
32	17	65.4	137	2	G71541 probable comp-depe
33	17	65.4	137	2	C81695 cyclic nucleotide-
34	17	65.4	156	2	S23357 H+-transporting tw
35	17	65.4	185	2	G64084 3-methyladenine DN
36	17	65.4	186	2	S66070 conserved hypothet
37	17	65.4	207	2	AC2950 transcription regu
38	17	65.4	213	2	H98332 probable transcrip
39	17	65.4	217	1	B64222 heat shock protein
40	17	65.4	223	2	H84977 ribose-5-phosphate
41	17	65.4	226	2	A86268 hypothetical prote
42	17	65.4	234	1	XCSN51 toxic shock syndro
43	17	65.4	234	2	B83992 toxic shock syndro
44	17	65.4	234	2	C69519 conserved hypothet
45	17	65.4	239	2	A83953 uridylylate kinase s

ALIGNMENTS

RESULT 1

T50261

conserved hypothetical protein SPAC890.05 with G-patch domain [Imported] - fission ye

C:Species: Schizosaccharomyces pombe

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

C:Accession: T50261

R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, December 1999

A:Reference number: Z25052

A:Accession: T50261

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-284 <S>A>

A:Cross-references: EMBL:AL133498; P1DN:CA63496.1; GSPDB:GN00066; SPDB:SPAC890.05

A:Experimental source: strain 972h(-); cosmid c890

C:Genetics:

A:Gene: SPDB:SPAC890.05

A:Map position: 1

Query Match

Best Local Similarity 73.1%; Score 19; DB 2; Length 284;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXXD 10

DB 179 KKTSTGSAID 188

RESULT 2

E84806 probable elongation factor [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: E84806

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beaulieu, M.L.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Venakou, S.E.; Umayam, L.; Tallon,

enus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; M0ID:20083487; PMID:10617197

A:Accession: E84806

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-378 <S>O>

A:Cross-references: GB:AE002093; NID:93786016; P1DN:AAC67362.1; GSPDB:GN00139

C:Genetics:

A:Gene: AC29385560

A:Map position: 2

Query Match

Best Local Similarity 73.1%; Score 19; DB 2; Length 378;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 ||
 Db 13 KKADAAALD 22

RESULT 3

R3LV14
 ribosomal protein S14, chloroplast - liverwort (Marchantia polymorpha) chloroplast
 C:Species: chloroplast Marchantia polymorpha
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999
 C:Accession: A02733, S01876

R:Ohama, K., submitted to the EMBL Data Library, October 1986

A:Reference number: A00150

A:Accession: A02733

A:Molecule type: DNA

A:Residues: 1-100 <OHY>

R:Ohama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umeson, K.; Shi

Nature 322, 572-574, 1986

A:Title: Chloroplast gene organization deduced from complete sequence of liverwort March

A:Reference number: A38014

A:Contents: annotation; gene organization, sites, features

R:Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T

J. Mol. Biol. 203, 299-331, 1988

A:Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gen

A:Reference number: S01567; MUID:89068686; PMID:2974085

A:Accession: S01876

A:Molecule type: DNA

A:Residues: 1-100 <UDME>

A:Cross-references: GB:X04465; GB:Y00686; NID:g11640; PIDN:CAA28083.1; PID:g11670

C:Genetics:

A:Gene: rps14

A:Genome: chloroplast

C:Superfamily: Escherichia coli ribosomal protein S14

C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 69.2%; Score 18; DB 1; Length 100;

Best Local Similarity 40.0%; Pred. No. 7.8;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 ||
 Db 29 KKTETSLD 38

RESULT 4

T48837
 hypothetical protein 68B2.210 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001

C:Accession: T48837

R:Schulze, U.; Altm, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24541

A:Accession: T48837

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-159 <SCH>

A:Cross-references: EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.210

A:Experimental source: cosmid contig 68B2; strain 74

C:Genetics:

A:Gene: NCSP:68B2.210

A:Map position: 2

C:Superfamily: Neurospora crassa hypothetical protein 68B2.210

Query Match 69.2%; Score 18; DB 2; Length 159;

Best Local Similarity 40.0%; Pred. No. 12;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 ||
 Db 71 KKTALQSLD 80

RESULT 5

A82401
 transcription regulator TetR family VCA0917 [imported] - Vibrio cholerae (strain N169

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: A82401

R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.

Charlson, D.; Ermolaeva, M.D.; Vamthyan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: A82401

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-161 <HEI>

A:Cross-references: GB:AE004420; GB:AE003853; NID:g9656361; PIDN:AAF96814.1; GSPDB:GN

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VCA0917

A:Map position: 2

Query Match 69.2%; Score 18; DB 2; Length 161;

Best Local Similarity 40.0%; Pred. No. 12;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 ||
 Db 62 KKTDFASALD 71

RESULT 6

S07748
 hypothetical protein 13 - Paramecium tetraurelia mitochondrion

C:Species: mitochondrion Paramecium tetraurelia

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-Dec-1999

C:Accession: S07748

R:Pritchard, A.E.; Sellmeier, J.J.; Mahalingam, R.; Sable, C.L.; Vennuti, S.E.; Cummin

Nucleic Acids Res. 18, 173-180, 1990

A:Title: Nucleotide sequence of the mitochondrial genome of Paramecium.

A:Reference number: S07725; MUID:90174913; PMID:2308823

A:Accession: S07748

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-169 <PRI>

A:Cross-references: EMBL:X15917; NID:g13256; PID:g578763

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

A:Start codon: ATA

C:Superfamily: Paramecium tetraurelia mitochondrion hypothetical protein 13

C:Keywords: mitochondrion

Query Match 69.2%; Score 18; DB 2; Length 169;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 ||
 Db 36 KKTSTYSKLD 45

RESULT 7

A96723
 hypothetical protein F20P5.23 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96723

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federopiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marshall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A96723

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <STO>

A:Cross-References: GB:AE005173; NID:g2194134; PIDN:AAB61109.1; GSPDB:GN00141

C:Genetics:

A:Gene: F20P5.23

A:Map position: 1

Query Match 69.2%; Score 18; DB 2; Length 171;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 16 KKLTTTDL 25

RESULT 8
C90786
Probable tet operon regulator [Imported] - *Escherichia coli* (strain O157:H7, substrain F)

C:Species: *Escherichia coli*

C>Date: 18-Jul-2001 #sequence-revision 18-Jul-2001 #text-change 18-Jul-2001

C:Accession: C90786

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: C90786

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <HAY>

A:Cross-References: GB:BA000007; PIDN:BBB34682.1; PID:g13360719; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECS1259

Query Match 69.2%; Score 18; DB 2; Length 212;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 20 KKAIIISALD 29

RESULT 9
A85646
Probable tet operon regulator ycdc [Imported] - *Escherichia coli* (strain O157:H7, substrain F)

C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence-revision 16-Feb-2001 #text-change 14-Sep-2001

C:Accession: A85646

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85646

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <STO>

A:Cross-References: GB:AE005174; NID:g12514373; PIDN:AA655629.1; GSPDB:GN00145; UMGCP:215

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: ycdc

Query Match 69.2%; Score 18; DB 2; Length 212;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 20 KKAIIISALD 29

RESULT 10
C64843
Probable transcription regulator ycdc - *Escherichia coli* (strain K-12)

C:Species: *Escherichia coli*

C>Date: 12-Sep-1997 #sequence-revision 17-Sep-1997 #text-change 01-Mar-2002

C:Accession: C64843

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64843

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <BLAT>

A:Cross-References: GB:AE000203; GB:U00096; NID:g1787248; PIDN:AAC74098.1; PID:g17872

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ycdc

C:Keywords: DNA binding; transcription regulation

F:39-58/Region: helix-turn-helix motif

Query Match 69.2%; Score 18; DB 2; Length 212;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 20 KKAIIISALD 29

RESULT 11
B64080
Hypothetical protein HI0601 - *Haemophilus influenzae* (strain Rd KW20)

C:Species: *Haemophilus influenzae*

C>Date: 18-Aug-1995 #sequence-revision 18-Aug-1995 #text-change 08-Oct-1999

C:Accession: B64080

R:Eisenschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: B64080

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <YIG>

A:Cross-References: GB:U32741; GB:L42023; NID:g1573582; PIDN:AAC22258.1; PID:g1573592

Query Match 69.2%; Score 18; DB 2; Length 217;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
|| ||
Db 161 KKSXGATLD 170

RESULT 12
T14770
Hypothetical protein DKFZP566E144.1 - human

C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000
 C:Accession: F37386
 R:Biocheck: H.; Boecher, M.; Brandt, P.; Nemes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: 218182
 A:Accession: F14770
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-237 <BLD>
 A:Cross-references: EMBL:AL110239
 A:Experimental source: fetal kidney; clone DKFZp566E144
 C:Genetics:
 A:Note: DKFZp566E144.1
 C:Superfamily: human conserved hypothetical protein DKFZp566E144.1

Query Match 69.2%; Score 18; DB 2; Length 237;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 || ||
 DB 189 KKAASHRALD 198

RESULT 13
 S01924
 hypothetical protein 6 - Chlamydia trachomatis plasmids
 N:Alternate names: hypothetical protein P-10
 C:Species: Chlamydia trachomatis
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Oct-1999
 C:Accession: S01924; S00794
 R:Commanducci, M.; Ricci, S.; Ratti, G.
 M.Ol. Microbiol. 2, 531-538, 1988
 A:Title: The structure of a plasmid of Chlamydia trachomatis believed to be required for
 A:Reference number: S01920; MUID:89013895; PMID:2845228
 A:Accession: S01924
 A:Molecule type: DNA
 A:Residues: 1-247 <CON>
 A:Cross-references: EMBL:X07547; NID:940730; PIDN:CAA30426.1; PID:g581014
 A:Experimental source: plasmid pCHL1
 A:Note: the authors translated the initiation codon GTG for residue 1 as Val
 R:Hatt, C.; Ward, M.E.; Clarke, I.N.
 Nucleic Acids Res. 16, 4053-4067, 1988
 A:Title: Analysis of the entire nucleotide sequence of the cryptic plasmid of Chlamydia
 A:Reference number: S00788; MUID:88233998; PMID:2836808
 A:Accession: S00794
 A:Molecule type: DNA
 A:Residues: 175-247 <HAT>
 A:Cross-references: EMBL:X06707
 A:Experimental source: plasmid pLGV440
 C:Genetics:
 A:Genome: Plasmid
 A:Start codon: GTG

Query Match 69.2%; Score 18; DB 2; Length 247;
 Best Local Similarity 40.0%; Pred. No. 18;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 || ||
 DB 13 KKNOTAAALD 22

RESULT 14
 F37386
 hypothetical protein 6 - Chlamydia trachomatis (serotype D) plasmid pCHL1
 C:Species: Chlamydia trachomatis
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Feb-1994
 C:Accession: F37386
 R:Commanducci, M.; Ricci, S.; Cevenini, R.; Ratti, G.
 Plasmid 23, 149-154, 1990
 A:Title: Diversity of the Chlamydia trachomatis common plasmid in biovars with different

A:Reference number: A37386; MUID:90301796; PMID:2194229
 A:Accession: F37386
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-247 <CON>
 A:Cross-references: GB:J03321
 C:Genetics:
 A:Genome: plasmid

Query Match 69.2%; Score 18; DB 2; Length 247;
 Best Local Similarity 40.0%; Pred. No. 18;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 || ||
 DB 13 KKNOTAAALD 22

RESULT 15
 AB3091
 hypothetical protein AtuA350 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AB3091
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavain, T.; Levy, R.; Li, M.; MCI
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tso, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AB3091
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-278 <KUP>
 A:Cross-references: GB:AE006689; PIDN:AAL45144.1; PID:g17742817; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: AtuA350
 A:Map position: Linear chromosome

Query Match 69.2%; Score 18; DB 2; Length 278;
 Best Local Similarity 40.0%; Pred. No. 20;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 || ||
 DB 184 KKLAAVHTLD 193

Search completed: June 5, 2003, 15:33:59
 Job time : 11.6485 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 5, 2003, 15:34:07 ; Search time 6.51515 Seconds

(without alignments)
63.661 Million cell updates/sec

Title: US-09-150-947F-14

Sequence: 1 KKKXXXXXKD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	100	1	RR14_MARPO
2	18	69.2	152	1	NIJ1_HUMAN
3	18	69.2	152	1	NIJ1_MOUSE
4	18	69.2	152	1	NIJ1_MOUSE
5	18	69.2	169	1	YMI3_PASTE
6	18	69.2	212	1	YCDC_ECOLI
7	18	69.2	217	1	TFOX_HAEIN
8	18	69.2	237	1	ORN_HUMAN
9	18	69.2	247	1	GPED_CHLTR
10	18	69.2	344	1	VPO_BBP2
11	18	69.2	365	1	FLC1_PROMI
12	18	69.2	413	1	Y349_MYCPN
13	18	69.2	427	1	ARP3_SCHPO
14	18	69.2	477	1	XYNA_STRLI
15	18	69.2	477	1	XYNA_STRLI
16	18	69.2	837	1	YL34_YEAST
17	18	69.2	1279	1	BCRH_CHLVI
18	18	69.2	1279	1	EXTS_PASMO
19	18	69.2	118	1	YQ93_CAEEL
20	18	69.2	143	1	NIJ2_HUMAN
21	18	69.2	143	1	NIJ2_MOUSE
22	18	69.2	144	1	NIJ2_MOUSE
23	18	69.2	147	1	ATP1_MYCGA
24	18	69.2	156	1	ATP1_ODOSI
25	18	69.2	185	1	YABF_HAEIN
26	18	69.2	186	1	YABF_BACST
27	18	69.2	211	1	ORN_DROME
28	18	69.2	217	1	GRPE_MYCGE
29	18	69.2	223	1	GRPE_MYCGE
30	18	69.2	234	1	GRPE_MYCGE
31	18	69.2	256	1	YB32_MYCPN
32	18	69.2	266	1	ETC2_STRAU
33	18	69.2	266	1	ETC2_STRAU

34	17	65.4	272	1	TRUB_CAMJE	09p12 campylobact
35	17	65.4	276	1	MYO1_ONCMY	091205 oncohyacin
36	17	65.4	307	1	ERA_NEIMA	09jv42 neisseria m
37	17	65.4	307	1	ERA_NEIMA	09k067 neisseria m
38	17	65.4	347	1	Y999_MYCPN	09m256 aspergillus
39	17	65.4	363	1	LE3A_ASPNG	09m256 aspergillus
40	17	65.4	368	1	DXR_HELPJ	09m256 aspergillus
41	17	65.4	390	1	CNX2_ARATH	09m256 arabidopsis
42	17	65.4	399	1	Y199_ARCFU	028380 archaeoglob
43	17	65.4	413	1	YB44_MYCPN	09m256 mycoplasma
44	17	65.4	457	1	PRIC_STRGR	09m256 streptococ
45	17	65.4	467	1	LEU2_ANASP	08yx02 anabaena sp

ALIGNMENTS

RESULT 1	ID	RR14_MARPO	STANDARD	PRT	100 AA
AC	P06370:				
DT	01-JAN-1988	(Rel. 06, Created)			
DT	01-JAN-1988	(Rel. 06, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Chloroplast 30S ribosomal protein S14.				
GN	RPS14.				
OS	Marchantia polymorpha (Liverwort).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;				
OC	Marchantiopsida; Marchantiales; Marchantiaceae; Marchantia.				
OX	NCBI_TaxID=3197;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85087956; PubMed=6393057;				
RA	Umesono K., Inokuchi H., Ohyama K., Ozeki H.;				
RT	Nucleotide sequence of Marchantia polymorpha chloroplast DNA: a				
RT	region possibly encoding three tRNAs and three proteins including a				
RT	homologue of E. coli ribosomal protein S14."				
RL	Nucleic Acids Res. 12:9551-9565(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.;				
RA	Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.;				
RA	Ozeki H.;				
RT	"Chloroplast gene organization deduced from complete sequence of				
RT	liverwort Marchantia polymorpha chloroplast DNA."				
RL	Nature 322:572-574(1986).				
CC	-1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: X01647; CA25805.1; -				
DR	EMBL: X04465; CA28083.1; -				
DR	PIR: A02733; R3LV14.				
DR	InterPro: IPR001209; Ribosomal_S14.				
DR	Pfam: PF00253; Ribosomal_S14.1.				
DR	PROSITE: PS00527; RIBOSOMAL_S14.1.				
KW	Ribosomal protein; chloroplast.				
SO	SEQUENCE 100 AA; 11880 MW; SABI4F809633EBD CRC64;				
QY	Query Match	69.2%;	Score 18;	DB 1;	Length 100;
	Best local Similarity	40.0%;	Pred. No. 4.4;		
	Matches	4;	Conservative	0;	Mismatches
				6;	Indels
					Gaps
					0;

DB 29 KKITSSLD 38

RESULT 2

NIJL_HUMAN STANDARD: PRT: 152 AA.

AC Q92982; Q92982; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Nijurin 1 (Nerve injury-induced protein 1).

GN NINJ1

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96374367; PubMed=8780658;

RA Araki T., Milbrandt J.;

RT "Ninjurin, a novel adhesion molecule, is induced by nerve injury and promotes axonal growth."

RL Neuron 17:353-361(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98126436; PubMed=9465296;

RA Chadwick B.P., Heath S.K., Williamson J., Obermayr F., Patel L., Sheer D., Frischauf A.M.;

RT "The human homologue of the ninjurin gene maps to the candidate region of hereditary sensory neuropathy type I (HSNI)."

RL Genomics 47:58-63(1998).

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Lung;

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP CHARACTERIZATION.

RX MEDLINE=97407927; PubMed=9261151;

RA Araki T., Zimonjic D.B., Popescu N.C., Milbrandt J.;

RT "Mechanism of homophilic binding mediated by ninjurin, a novel widely expressed adhesion molecule."

RL J. Biol. Chem. 272:21373-21380(1997)

CC -1- FUNCTION: HOMOPHILIC CELL ADHESION MOLECULE THAT PROMOTES AXONAL GROWTH. MAY PLAY A ROLE IN NERVE REGENERATION AND IN THE FORMATION AND FUNCTION OF OTHER TISSUES. CELL ADHESION REQUIRES DIVALENT CATIONS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN BOTH ADULT AND EMBRYONIC TISSUES, PRIMARILY THOSE OF EPITHELIAL ORIGIN.

CC -1- INDUCTION: BY NERVE INJURY BOTH IN DORSAL ROOT GANGLION NEURONS AND IN SCHWANN CELLS.

CC -1- SIMILARITY: BELONGS TO THE NINJURIN FAMILY.

CC -----

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CC -----

CC EMBL; U72661; AAB1560.1; -

DR EMBL; U91512; AAC14593.1; -

DR EMBL; AF029251; AAC39574.1; -

DR EMBL; BC004440; AA04440.1; -

DR Genew: HGNC:7824; NINJ1.

DR MIM; 602062; -

DR Cell adhesion; Transmembrane.

FT DOMAIN 1 80 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 81 101 POTENTIAL.

FT DOMAIN 102 120 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 121 141 POTENTIAL.

FT DOMAIN 142 152 EXTRACELLULAR (POTENTIAL).

FT CONFLICT 110 110 D -> A (IN REF. 3).

SO SEQUENCE 152 AA; 16389 MW; FEACAD8001597855 CRC64;

Query Match

Best Local Similarity 40.0%; Score 18; DB 1; Length 152;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXLD 10

DB 44 KKAASMD 53

RESULT 3

NIJL_MOUSE STANDARD: PRT: 152 AA.

AC Q70131;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ninjurin 1 (Nerve injury-induced protein 1).

GN NINJ1

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98126436; PubMed=9465296;

RA Chadwick B.P., Heath S.K., Williamson J., Obermayr F., Patel L., Sheer D., Frischauf A.M.;

RT "The human homologue of the ninjurin gene maps to the candidate region of hereditary sensory neuropathy type I (HSNI)."

RL Genomics 47:58-63(1998).

RN [2]

RP SEQUENCE FROM N.A.

RX Moon A.R., Kim J.W., Hong Y.M., Oh G.T., Chang S.Y., Lee K.S., Choe I.S.;

RT "Mus musculus ninjurin genomic DNA."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: HOMOPHILIC CELL ADHESION MOLECULE THAT PROMOTES AXONAL GROWTH. MAY PLAY A ROLE IN NERVE REGENERATION AND IN THE FORMATION AND FUNCTION OF OTHER TISSUES. CELL ADHESION REQUIRES DIVALENT CATIONS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- INDUCTION: BY NERVE INJURY.

CC -1- SIMILARITY: BELONGS TO THE NINJURIN FAMILY.

CC -----

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CC -----

CC EMBL; U91513; AAC14594.1; -

DR EMBL; AF219626; AAC32161.1; -

DR MGD; MGI:1196617; Nlnj1.

DR Cell adhesion; Transmembrane.

FT DOMAIN 1 79 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 80 100 POTENTIAL.

FT DOMAIN 101 120 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 121 141 POTENTIAL.

FT DOMAIN 142 152 EXTRACELLULAR (POTENTIAL).

SO SEQUENCE 152 AA; 16555 MW; E261CB447BC0A2E6 CRC64;

Query Match

Best Local Similarity 69.2%; Score 18; DB 1; Length 152;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXLD 10

DB 44 KKSAAESMD 53

RESULT 4

ID NINJ1_RAT STANDARD; PRT; 152 AA.

AC P10617;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ninturin 1 (Nerve injury-induced protein 1).

GN NINJ1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96374367; PubMed=8780658;

RA Araki T., Milbrandt J.;

RT "Ninturin, a novel adhesion molecule, is induced by nerve injury and promotes axonal growth."

RL Neuron 17:353-361(1998).

CC -1- FUNCTION: HOMOPHILIC CELL ADHESION MOLECULE THAT PROMOTES AXONAL GROWTH. MAY PLAY A ROLE IN NERVE REGENERATION AND IN THE FORMATION AND FUNCTION OF OTHER TISSUES. CELL ADHESION REQUIRES DIVALENT CATIONS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO THE NINTURIN FAMILY.

CC -----

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CC -----

DR EMBL: U72660; AAB17559.1; -

KW Cell adhesion; Transmembrane.

FT DOMAIN 1 79 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 80 100 POTENTIAL.

FT DOMAIN 101 120 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 121 141 POTENTIAL.

FT DOMAIN 142 152 EXTRACELLULAR (POTENTIAL).

SO SEQUENCE 152 AA; 16539 MW; 414B3BDBE1807E80 CRC64;

Query Match 69.2%; Score 18; DB 1; Length 152;

Best local Similarity 40.0%; Pred. No. 6.5;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXID 10

DB 44 KKSAAESMD 53

RESULT 5

ID YMI3_PART2 STANDARD; PRT; 169 AA.

AC P15614;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-APR-1990 (Rel. 14, Last annotation update)

DE Hypothetical 20.2 kDa protein (ORF13).

OS Parametrium tetrarella.

OC Mitochondrion.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Pericollata; Parametrium.

OX NCBI_TaxID=5888;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Stock 51;

RX MEDLINE=90174913; PubMed=2308823;

RA Pritchard A.E., Sellhammer J.J., Mahalingam R., Sable C.L.,

RA Venuti S.E., Cummings D.J.;

RT "Nucleotide sequence of the mitochondrial genome of Parametrium."

RL Nucleic Acids Res. 18:1173-180(1990).

CC -----

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CC -----

DR EMBL: X15917; CAA34057.1; -

DR PIR: S07748; S07748.

KW Hypothetical protein; Mitochondrion.

SO SEQUENCE 169 AA; 20303 MW; D991AD99A8EBA174 CRC64;

Query Match 69.2%; Score 18; DB 1; Length 169;

Best local Similarity 40.0%; Pred. No. 7.2;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXID 10

DB 36 KKTSTYSKID 45

RESULT 6

ID YCDC_ECOLI STANDARD; PRT; 212 AA.

AC P75899;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical transcriptional regulator ycdc.

GN YCDC OR B1013.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

RA "The complete genome sequence of Escherichia coli K-12."

RL Science 277:1453-1474(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikeno K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horuchi T.;

RA "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."

RL DNA Res. 3:137-155(1996).

CC -1- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.

CC -----

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or send an email to license@lsb.sib.ch).

CC -----

DR EMBL: AE000203; AAC74098.1; -

DR EMBL: D90738; BAA35790.1; -

DR Ecogene: EG12301; YC6C.

DR InterPro: IPR001647; HTM_Tetr.

DR Pfam: PF00440; tetr.1.

DR PROSITE: PS01081; HTM_TETR_FAMILY; FALSE_NEG.

KW Hypothetical protein; Transcription regulation; DNA-binding;

KM Complete proteome.

FT DNA_BIND 39 58 H-T-H MOTIF (POTENTIAL).

SO SEQUENCE 212 AA: 23687 MW; E245985DFAC277A CRC64;

Query Match 69.2%; Score 18; DB 1; Length 212;

Best Local Similarity 40.0%; Pred. No. 9;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

DB 20 KKAISALD 29

RESULT 7

TFOX_HAEIN STANDARD; PRT; 217 AA.

AC P43779;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE DNA transformation protein tfox (Competence activator) (Protein sxy).

GN TFOX OR SXY OR HT0601.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OX Haemophilus.

OX NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Rd:

RX MEDLINE=95241551; PubMed=7724607;

RA Zully J.J., Barcak G.J.;

RT "Identification of a DNA transformation gene required for com101A+ expression and supertransformer phenotype in Haemophilus influenzae";

RT Proc. Natl. Acad. Sci. U.S.A. 92:3616-3620(1995).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN-Rd / KW20 / ATCC 51907;

RC MEDLINE=95350630; PubMed=7542800;

RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kesteven K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., McInerney K., Shiley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C., Fine L.D., Fritchman J.L., Furmann J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;

RA "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

RT Science 269:496-512(1995).

RL [3]

RN IDENTIFICATION OF TFOX AS SXY AND VARIANT SXY-1.

RX MEDLINE=95050244; PubMed=7961436;

RA Williams P.M., Bannister L.A., Redfield R.J.;

RT "The Haemophilus influenzae sxy-1 mutation is in a newly identified gene essential for competence";

RT J. Bacteriol. 176:6789-6794(1994).

CC -1- FUNCTION: REQUIRED FOR DNA TRANSFORMATION. POSITIVELY REGULATES GENES REQUIRED FOR DNA TRANSFORMATION (LATE COMPETENCE-SPECIFIC GENES).

CC -1- SIMILARITY: TO E.COLI YCCR.

CC -----

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CC -----

DR EMBL: U13205; AAC43320.1; -

DR EMBL: U13205; AAC43321.1; -

DR EMBL: U32741; AAC22258.1; -

DR TIGR: HT0601; -

KW Competence; Transcription regulation; Activator;

KM Alternative initiation; Complete proteome.

FT CHAIN 1 217 DNA TRANSFORMATION PROTEIN TFOX.

FT CHAIN 40 217 DNA TRANSFORMATION PROTEIN TFOX-SHORT.

FT INIT MET 40 40 FOR TFOX-SHORT.

FT VARIANT 19 19 V -> I (IN SXY-1; CAUSES A 100 x TO 1000 X INCREASE IN SPONTANEOUS NATURAL COMPETENCE).

FT W -> L (IN REF. 1).

FT CONFLICT 203 203

SO SEQUENCE 217 AA: 25074 MW; 4A6E30E64008CC3F CRC64;

Query Match 69.2%; Score 18; DB 1; Length 217;

Best Local Similarity 40.0%; Pred. No. 9.2;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

DB 161 KKSQSGATLD 170

RESULT 8

ORN_HUMAN STANDARD; PRT; 237 AA.

AC Q9Y3B8; Q9UFY7;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Oligoribonuclease, mitochondrial precursor (EC 3.1.1.-) (Small fragment nuclease) (CGI-114).

GN SFN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (SHORT ISOPORM).

RX MEDLINE=20272150; PubMed=10810093;

RA Lai C.-H., Chou C.-Y., Chang L.-Y., Liu C.-S., Lin W.-C.;

RT "Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics";

RT Genome Res. 10:703-713(2000).

RL [2]

RN SEQUENCE FROM N.A. (LONG ISOPORM).

RP TISSUE-Kidney.

RC MEDLINE=21154917; PubMed=11230166;

RX Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecker M., Bloeker H., Baurenschs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Ousmaka A.;

RA "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs";

RT Genome Res. 11:422-435(2001).

RL [3]

RN CHARACTERIZATION.

RX MEDLINE=20408924; PubMed=10851236;

RA Nguyen L.H., Erzberger J.P., Root D.M. III;

RT "The human homolog of Escherichia coli Orn degrades small single-stranded RNA and DNA oligomers";

RT J. Biol. Chem. 275:25900-25906(2000).

CC -1- FUNCTION: 3'-TO-5' EXORIBONUCLEASE SPECIFIC FOR SMALL OLIGORIBONUCLEOTIDES. CC ACTIVE ON SMALL (PRIMARYLY </=5

CC NUCLEOTIDES IN LENGTH) SINGLE-STRANDED RNA AND DNA OLIGOMERS. MAY
 CC HAVE A ROLE FOR CELLULAR NUCLEOTIDE RECYCLING.
 CC -1- COFACTOR: MANGANESE.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (LONG ISOFORM) AND NUCLEAR
 CC (SHORT ISOFORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/SPN-ALPHA (SHOWN
 CC HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE OLIGORIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF151872; AAD34109.1; -
 DR EMBL; AL110239; CAB53690.1; -
 DR InterPro: IPR000520; Exonuclease.
 DR Pfam: PF00929; Exonuclease; 1.
 DR SMART; SM00479; EXOIII; 1.
 KW Hydroxylase; Exonuclease; Nuclease; Mitochondrion; Transit peptide;
 KW Nuclear protein; Manganese; Alternative splicing.
 FT TRANSIT 1
 FT CHAIN ? 237 MITOCHONDRION (POTENTIAL).
 FT ACT_SITE 164 164 POTENTIAL.
 FT VARSPIC 1 38 MISSING (IN ISOFORM 2).
 FT MUTAGEN 168 168 D->A: ABOLISHES ACTIVITY.
 FT CONFLICT 103 103 R -> K (IN REF. 1).
 FT SEQUENCE 237 AA; 26861 MW; BF093A89078C138F CRC64;
 SO
 Query Match 69.2%; Score 18; DB 1; Length 237;
 Best Local Similarity 40.0%; Pred. NO. 10;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 KKKXXXXXD 10
 DB 189 KKAASHRALD 198
 RESULT 9
 GPE6.CHLTR
 ID GPE6.CHLTR STANDARD; PRT; 247 AA.
 AC P10560; P08787; Q66433;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Virulence plasmid protein pGP6-D (Protein P-10).
 DE Chlamydia trachomatis.
 OS Plasmid pLGVA40, Plasmid pCHL1, and Plasmid pCTT1.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L2/434/Bu; PLASMID-pLGVA40;
 RX MEDLINE=89013895; PubMed=2845228;
 RA Comanducci M., Ricci S., Ravetti G.,
 RT "The structure of a plasmid of Chlamydia trachomatis believed to be
 RT required for growth within mammalian cells.";
 RL Mol. Microbiol. 2:531-538(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L1/440/LN; PLASMID-pLGVA40;
 RX MEDLINE=8623398; PubMed=2836808;
 RA Hatt C., Ward M.E., Clarke I.N.,
 RT "Analysis of the entire nucleotide sequence of the cryptic plasmid of
 RT Chlamydia trachomatis serovar L1. Evidence for involvement in DNA
 RT replication.";
 RL Nucleic Acids Res. 16:4053-4067(1988).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN-G0/86 / Serotype D; PLASMID-pCHL1;
 RX MEDLINE=90301796; PubMed=2194229;
 RA Comanducci M., Ricci S., Cevenini R., Ravetti G.;
 RT "Diversity of the Chlamydia trachomatis common plasmid in biovars
 RT with different pathogenicity.";
 RL Plasmid 23:149-154(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Serotype B; PLASMID-pCTT1;
 RX MEDLINE=88177106; PubMed=3444859;
 RA Stripakash K.S., Macavoy E.S.,
 RT "Characterization and sequence of a plasmid from the trachoma biovar
 RT of Chlamydia trachomatis.";
 RL Plasmid 18:205-214(1987).
 CC -1- MISCELLANEOUS: pGP6-D IS REQUIRED FOR GROWTH WITHIN MAMMALIAN
 CC CELLS.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF PLASMID pLGVA40.
 CC -1- SIMILARITY: BELONGS TO THE UPF0137 (pGP6-D) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X07547; CAA30426.1; -
 DR EMBL; X06707; CAA29897.1; -
 DR EMBL; J03321; AAA91574.1; -
 DR EMBL; M19487; AAB02591.1; -
 DR PIR; S01924; S01924.
 DR PIR; S00794; S00794.
 DR InterPro: IPR005350; UPF0137.
 DR Pfam: PF03677; UPF0137; 1.
 KW Plasmid.
 FT VARIANT 9 9 N -> D (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 47 47 Q -> R (IN PLASMIDS PCHL1 AND PCTT1).
 FT VARIANT 183 186 VLDO -> CMIE (IN PLASMID PCTT1).
 FT VARIANT 194 194 K -> T (IN PLASMID PCTT1).
 FT VARIANT 205 205 S -> L (IN PLASMID PCTT1).
 FT VARIANT 222 222 M -> I (IN PLASMID PCTT1).
 FT SEQUENCE 247 AA; 28307 MW; F1FA11F29037C221 CRC64;
 SO
 Query Match 69.2%; Score 18; DB 1; Length 247;
 Best Local Similarity 40.0%; Pred. NO. 10;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 KKKXXXXXD 10
 DB 13 KKNQTAASLD 22
 RESULT 10
 VPO_BPP2
 ID VPO_BPP2 STANDARD; PRT; 344 AA.
 AC P25480;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Presumed portal vertex protein (GPO).
 DE O.
 OS Bacteriophage P2.
 OC viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P2-like viruses.
 OX NCBI_Taxid=10679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=92115571; PubMed=1837355;
 RX Linderoth N.A., Ziemann R., Hagggaard-Ljungquist E., Christie G.E.,
 RA Calendar R.,
 RT "Nucleotide sequence of the DNA packaging and capsid synthesis genes
 RT of bacteriophage P2.";

RL Nucleic Acids Res. 19:7207-7214(1991).
 CC -1- FUNCTION: THE Q, P AND M PROTEINS ARE NEEDED TO PACKAGE DNA INTO
 CC PROHEADS AND FOR THE CONVERSION OF PROHEADS TO CAPSIDS.
 CC -1- SIMILARITY: STRONG, TO PHAGE HP1 PROTEIN ORF15 AND TO THE E. COLI
 CC HYPOTHETICAL 36.8 kDa PROTEIN (ORF5) IN RETRON EC67.
 CC -----
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 CC -----
 DR EMBL; AF063097; AAD03268.1; --
 DR PIR; S16410; S16410.
 DR PIR; S22796; S22796.
 KW Capsid assembly.
 SQ SEQUENCE 344 AA; 39114 MW; FAD61987530029A7 CRC64;
 Query Match 69.2%; Score 18; DB 1; Length 344;
 Best Local Similarity 40.0%; Pred. No. 14;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KKKXXXXXD 10
 DB 270 KKASADLD 279
 RESULT 11
 FLCL PROMT STANDARD; PRT; 365 AA.
 ID FLCL_PROMT
 AC P42272;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Flagellin 1.
 GN FLICL.
 OS Proteus mirabilis.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Proteus.
 CC NCB1_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-29.
 RC STRAIN-BB200;
 RX MEDLINE-95011656; PubMed-7926835;
 RA Belas R., Flaherty D.;
 RT "Sequence and genetic analysis of multiple flagellin-encoding genes
 RT from Proteus mirabilis.";
 RL Gene 148:33-41(1994).
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
 CC -1- INDUCTION: ALTHOUGH SWIMMER CELLS HAVE ONLY A FEW FLAGELLA, THE
 CC ELONGATED SWARMER CELLS ARE PROPELLED COVERED BY THOUSANDS OF NEW
 CC FLAGELLA SYNTHESIZED SPECIFICALLY IN RESPONSE TO GROWTH ON
 CC SURFACES OR IN HIGHLY VISCOUS LIQUIDS.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF221556; AAB62396.1; --
 DR InterPro; IPR001492; Flagellin.
 DR InterPro; IPR001029; Flagellin_C.
 DR Pfam; PF00669; Flagellin_N.1.
 DR Pfam; PF00700; Flagellin_C.1.
 DR PRINTS; PR00207; Flagellin.
 DR PRD000; PD000316; Flagellin_C.1.

KW Flagella; Multigene family.
 SQ SEQUENCE 365 AA; 39093 MW; 2A23106F040DB522 CRC64;
 Query Match 69.2%; Score 18; DB 1; Length 365;
 Best Local Similarity 40.0%; Pred. No. 15;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KKKXXXXXD 10
 DB 197 KKNAAATLD 206
 RESULT 12
 Y349_MYCPN STANDARD; PRT; 413 AA.
 ID Y349_MYCPN
 AC P75253;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG349 homolog (G12_orf413).
 GN MPN525 OR MP317.
 OS Mycoplasma pneumoniae.
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 CC NCB1_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE-97105885; PubMed-8948633;
 RA Himmelfeich R., Hiltbert H., Plagens H., Pirk E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE000029; AAB95965.1; --
 DR KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 413 AA; 48246 MW; AACFC2C9802316F23 CRC64;
 Query Match 69.2%; Score 18; DB 1; Length 413;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KKKXXXXXD 10
 DB 10 KKATFSGLD 19
 RESULT 13
 ARP3_SCHPO STANDARD; PRT; 427 AA.
 ID ARP3_SCHPO
 AC P32390;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Actin-like protein 3.
 GN ACT2 OR SPAC630.03.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCB1_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-92108083; PubMed-1729722;
 RX Lees-Miller J.P., Henry G., Helfman D.M.;

*Identification of act2, an essential gene in the fission yeast
Schizosaccharomyces pombe that encodes a protein related to actin.
Proc. Natl. Acad. Sci. U.S.A. 89:80-83(1992).
[2]
SEQUENCE FROM N.A.
RC STRAIN-972; PubMed-11859360;
MEDLINE-21848401; PubMed-11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras K., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher S.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leach S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Wellens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerruti L., Love T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Useary D., Barrett B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- FUNCTION: PART OF A COMPLEX IMPLICATED IN THE CONTROL OF ACTIN
POLYMERIZATION IN CELLS (BY SIMILARITY). MAY BE INVOLVED IN
CYTOKINESIS.
CC -1- SUBUNIT: BELONGS TO A COMPLEX COMPOSED OF ARP2, ARP3, P41-ARC,
P34-ARC, P21-ARC, P20-ARC AND P16-ARC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY. ARP3 SUBFAMILY.
CC -----
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CC -----
CC EMBL: M81068; NOT_ANNOTATED_CDS.
DR EMBL: AL109832; CAB52725.1; -.
DR PIR: A41790; A41790.
DR InterPro: IPR004000; Actin_like.
DR Pfam: PF000022; actin; 1.
DR SMART: SM00268; ACTIN; 1.
DR PROSITE: PS01132; ACTIN_ACT-LIKE; 1.
KW Structural protein; Cytoskeleton.
SQ SEQUENCE 427 AA; 47373 MW; C7909FEFE544789B CRC64;
Query Match Score 2%; Score 18; DB 1; Length 427;
Best Local Similarity 40.0%; Pred. No. 17;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 KKKKXXXXX 10
DB 82 KKASAGSYLD 91
RESULT 14
ID XYNL STRLI STANDARD; PRT; 477 AA.
AC P26514; P96464;
DT 01-AUG-1992 (Rel. 23. Created)
DT 30-MAY-2000 (Rel. 39; Last sequence update)

15-JUN-2002 (Rel. 41; Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
GN (1,4-beta-D-xylan xylanohydrolase A).
OS XLANA.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinobacteriales;
OC Actinomycetales; Streptomycineae; Streptomyces.
OX NCBI_Taxid=1916;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 42-92.
RC STRAIN-66 / 1326;
RA MEDLINE-92077439; PubMed-1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans."
RL gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 20 AND 140-141.
RC STRAIN-66 / 1326;
RA Shareck F.;
RN Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
[3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.
RX MEDLINE-94342232; PubMed-8063693;
RA Derwenda U., Swenson L., Green R., Wei Y.Y., Morosoli R., Shareck F.,
RA Kluepfel D., Derwenda L.S.;
RT "Crystal structure, at 2.6-A resolution, of the Streptomyces lividans
RT xylanase A, a member of the F family of beta-1,4-D-glycanases."
RL J. Biol. Chem. 269:20811-20814(1994).
CC -1- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS. XLANA AND XLAN SEM TO ACT
CC SEQUENTIALLY ON THE SUBSTRATE TO YIELD XYLOBIOSE AND XYLOSE
CC AS CARBON SOURCES.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
CC -----
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CC -----
CC EMBL: M64551; AAC26525.1; -.
DR PIR: J50589; J50589.
DR PDB: 1XAS; 31-MAY-95.
DR InterPro: IPR001000; Glyco_hydro_10.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00652; Ricin_B_lectin; 3.
DR PRINTS: PR00134; GLHYDLASE10.
DR SMART: SM00458; RICIN; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS50231; RICIN_B_LLECTIN; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KW 3D-structure.
FT SIGNAL 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
FT ACT_SITE 169 169 PROTON DONOR.
FT ACT_SITE 277 277 NUCLEOPHILE.
SQ SEQUENCE 477 AA; 51162 MW; E14A7FE37BDC68CC CRC64;
Query Match Score 2%; Score 18; DB 1; Length 477;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 330 KKAAYTAVLD 339

RESULT 15
 YL34_YEAST

YL34_YEAST STANDARD: PRT: 837 AA.

AC 007844;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 93.1 kDa protein YL034C.
 GN YL034C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.

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 CC -----

CC
 DR EMBL: Z73139; CA97483.1; -
 DR SGD: S0003957; YL034C.
 DR InterPro: IPR003959; AAA_ATPase.
 DR InterPro: IPR003959; AAA_ATPase_cent.
 DR InterPro: IPR003960; AAA_sub.
 DR Pfam: PF00004; AAA; 2.
 DR SMART: SM00362; AAA; 2.
 DR PROSITE: PS00674; AAA; 1.
 KW Hypothetical protein; ATP-binding; Repeat.
 FT NP_BIND 246 253 ATP (POTENTIAL).
 FT NP_BIND 574 581 ATP (POTENTIAL).
 SO SEQUENCE 837 AA; 93069 MW; 133528B9D0987103 CRC64;

Query Match 69.2%; Score 18; DB 1; Length 837;
 Best Local Similarity 40.0%; Pred. No. 33;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 7 KKNLSLTSILD 16

Search completed: June 5, 2003, 15:56:33
 Job time : 8.51515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:32:58 ; Search time 29.0909 Seconds
(without alignments)
70.829 Million cell updates/sec

Title: US-09-150-947F-14
Perfect score: 26
Sequence: 1 KKKXXXXXXLD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	73.1	284	3	09URX9
2	19	73.1	378	10	09ZVH8
3	19	73.1	378	10	08VXZ6
4	19	73.1	1365	12	037174
5	19	73.1	1365	12	065005
6	19	73.1	1365	12	080248
7	18	69.2	46	2	09ZG37
8	18	69.2	108	2	08RTC9
9	18	69.2	153	2	09ANS7
10	18	69.2	160	4	08WUV5
11	18	69.2	161	16	09RL32
12	18	69.2	171	10	004541
13	18	69.2	205	11	09D854
14	18	69.2	212	16	08X4Z7
15	18	69.2	215	5	096609
16	18	69.2	276	8	P92729

17	18	69.2	278	16	08U709	08U709 agrobacteri
18	18	69.2	292	11	08RIE2	08RIE2 mus musculu
19	18	69.2	357	15	090FU8	090FU8 human immun
20	18	69.2	371	15	090K19	090K19 human immun
21	18	69.2	376	12	056872	056872 gallid herp
22	18	69.2	385	15	098273	098273 human immun
23	18	69.2	543	5	044130	044130 caenorhabdi
24	18	69.2	663	8	09MJ69	09MJ69 physarum po
25	18	69.2	716	2	09REY3	09REY3 carnobacter
26	18	69.2	716	2	046317	046317 carnobacter
27	18	69.2	716	2	0930C9	0930C9 carnobacter
28	18	69.2	765	4	0969N7	0969N7 homo sapien
29	18	69.2	765	4	0969Q7	0969Q7 homo sapien
30	18	69.2	796	4	096L97	096L97 homo sapien
31	18	69.2	841	2	044207	044207 agrobacteri
32	18	69.2	858	5	021853	021853 caenorhabdi
33	18	69.2	863	16	097LND	097LND clostridium
34	18	69.2	954	5	096Q15	096Q15 giardia lam
35	18	69.2	969	5	090022	090022 giardia lam
36	18	69.2	1032	5	019818	019818 caenorhabdi
37	18	69.2	1035	5	021380	021380 caenorhabdi
38	18	69.2	1117	5	08T1U6	08T1U6 dictyostell
39	18	69.2	1271	2	093SV9	093SV9 chlorobium
40	17	65.4	72	3	096726	096726 lutomyia l
41	17	65.4	109	17	028686	028686 archaeglob
42	17	65.4	119	17	0975E7	0975E7 sulfolobus
43	17	65.4	137	16	09PKF9	09PKF9 chlamydia m
44	17	65.4	137	16	084238	084238 chlamydia t
45	17	65.4	145	5	08SWF8	08SWF8 encephalit

ALIGNMENTS

RESULT 1	ID	Q9URX9	PRELIMINARY:	PRT:	284 AA.
AC	Q9URX9;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	Hypothetical 31.9 kDa protein C890.05 in chromosome I.				
GN	SPAC890.05.				
OS	Schizosaccharomyces pombe (fission yeast).				
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;				
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;				
OC	Schizosaccharomyces.				
OX	NCBI_TaxID=4896;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=972;				
RA	Saunders D., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G.,				
RL	Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.				
DR	EMBL: AL133498; CAB63496.1; -				
DR	InterPro: IPR000467; G_patch.				
DR	Pfam: PF01585; G_patch; 1.				
DR	SMART: SM00443; G_patch; 1.				
KW	Hypothetical protein.				
FT	DOMAIN 197..201				
FT	POLY-LYS.				
FT	DOMAIN 225..233				
FT	POLY-LYS.				
SQ	SEQUENCE 284 AA: 31878 MM: A1DF1ADDE2FA0235 CRC64:				
Query Match	73.1% Score 19; DB 3; Length 284;				
Best Local Similarity	40.0% Pred. No. 20;				
Matches	4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	1 KKKXXXXXXLD 10				
DB	179 KKTSGSALD 188				
RESULT 2	Q9ZVH8				

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ID 092VH8 PRELIMINARY; PRT; 378 AA.
AC 092VH8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative elongation factor.
GN AT2G38560.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005499; AAC67362.1;
DR HSSP; P23193; 1TF1.
DR InterPro; IPR001222; TFIIS.
DR InterPro; IPR003618; TFS2_centre.
DR InterPro; IPR003617; TFS2_N.
DR Pfam; PF01096; TFIIS; 1.
DR SMART; SM00510; TFS2M; 1.
DR SMART; SM00509; TFS2N; 1.
DR SMART; SM00440; ZNF_C2C2; 1.
DR PROSITE; PS00466; TFIIS; 1.
KM Elongation factor.
SQ SEQUENCE 378 AA; 41979 MW; 9A176DC31FA8E885 CRC64;

Query Match
Best Local Similarity 73.1%; Score 19; DB 10; Length 378;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 13 KKAADAAALD 22

RESULT 3
08VXZ6 PRELIMINARY; PRT; 378 AA.
ID 08VXZ6;
AC 08VXZ6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative elongation factor.
GN AT2G38560.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Tortum M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

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RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene At2g38560 (GI:15224901).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074322; AAL67018.1;
DR InterPro; IPR001222; TFIIS.
DR InterPro; IPR003618; TFS2_centre.
DR InterPro; IPR003617; TFS2_N.
DR Pfam; PF01096; TFIIS; 1.
DR SMART; SM00510; TFS2M; 1.
DR SMART; SM00509; TFS2N; 1.
DR SMART; SM00440; ZNF_C2C2; 1.
DR PROSITE; PS00466; TFIIS; UNKNOWN_1.
KM Elongation factor.
SQ SEQUENCE 378 AA; 42011 MW; 04E5E924FBD9CDB CRC64;

Query Match
Best Local Similarity 73.1%; Score 19; DB 10; Length 378;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 13 KKAADAAALD 22

RESULT 4
037174 PRELIMINARY; PRT; 1365 AA.
ID 037174;
AC 037174;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Replicase.
OS Bamboo mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=35286;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao J.T., Hsu Y.H.;
RT "Full-length sequence of infectious bamboo mosaic virus genomic RNA.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF018156; AAB70562.1;
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
SQ SEQUENCE 1365 AA; 155219 MW; CA54DBF5997F158A CRC64;

Query Match
Best Local Similarity 73.1%; Score 19; DB 12; Length 1365;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10
DB 1302 KKTATAYALD 1311

RESULT 5
065005 PRELIMINARY; PRT; 1365 AA.
ID 065005;
AC 065005;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF1-155K.
OS Bamboo mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=35286;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-BAMV-O;
 RA Hsu Y.-H.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BAMV-O;
 RX MEDLINE-94358760; PubMed-8077956;
 RA Lin N., Lin B., Lo N., Hu C., Chow T., Hsu Y.;
 RT "Nucleotide sequence of the genomic RNA of bamboo mosaic potexvirus.";
 RL J. Gen. Virol. 75:2513-2518(1994).
 DR EMBL: D26017; BAA05033.1; -
 DR InterPro: IPR001788; RNA_dep_RNAPol2.
 DR InterPro: IPR000606; Viral_helicase1.
 DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
 DR Pfam: PF01443; Viral_helicase1; 1.
 SQ SEQUENCE 1365 AA; 155129 MW; 35449D5E8026633 CRC64;

Query Match 73.1%; Score 19; DB 12; Length 1365;
 Best Local Similarity 40.0%; Pred. No. 79;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 1302 KKTATAYALD 1311

RESULT 6
 ID 08U248 PRELIMINARY; PRT; 1365 AA.
 AC 08U248;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative, putative, putative, putative, and putative genes.
 OS Bamboo mosaic virus
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 OX NCBI_Taxid=35286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BAMV-V;
 RA Yang C.-C., Liu J.-S., Lin C.-P., Lin N.-S.;
 RT "Nucleotide sequence and phylogenetic analysis of a bamboo mosaic
 RT potexvirus isolate from common bamboo (Bambusa vulgaris McClure).";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L77962; AAL4030.1; -
 DR InterPro: IPR001788; RNA_dep_RNAPol2.
 DR InterPro: IPR000606; Viral_helicase1.
 DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
 DR Pfam: PF01443; Viral_helicase1; 1.
 SQ SEQUENCE 1365 AA; 155222 MW; B542C00E2ECFC990 CRC64;

Query Match 73.1%; Score 19; DB 12; Length 1365;
 Best Local Similarity 40.0%; Pred. No. 79;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 1302 KKTATAYALD 1311

RESULT 7
 ID 09ZG37 PRELIMINARY; PRT; 46 AA.
 AC 09ZG37;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 5.2 kDa protein (Fragment).
 OS Chlamydia trachomatis.
 OG Plasmid pCH1.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF087330; AAD04105.1; -
 DR InterPro: IPR005350; UPF0137.
 DR Pfam: PF03677; UPF0137; 1.
 KW Hypothetical protein; Plasmid.
 FT NON_TER 1 46 1
 FT NON_TER 1 46 1
 SQ SEQUENCE 46 AA; 5214 MW; D2FDAC41C1960867 CRC64;

Query Match 69.2%; Score 18; DB 2; Length 46;
 Best Local Similarity 40.0%; Pred. No. 12;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 21 KKNQTAAASLD 30

RESULT 8
 ID 08RTC9 PRELIMINARY; PRT; 108 AA.
 AC 08RTC9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative portal vertex protein GPQ (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHO14;
 RA Pradel N., Leroy-Setrin S., Lévrel V.;
 RT "Sequences from Shiga toxin-producing Escherichia coli O91:H21."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF467512; AAL78348.1; -
 FT NON_TER 1 108 1
 FT NON_TER 1 108 1
 SQ SEQUENCE 108 AA; 12028 MW; 350B505A7A03B5B5 CRC64;

Query Match 69.2%; Score 18; DB 2; Length 108;
 Best Local Similarity 40.0%; Pred. No. 25;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXLD 10
 DB 54 KKSADLDD 63

RESULT 9
 ID 09ANS7 PRELIMINARY; PRT; 153 AA.
 AC 09ANS7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE LuxT.
 OS Vibrio parvulus.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
 OX NCBI_Taxid=669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Iin Y.H., Miyamoto C.M., Melghe E.A.;
 RT "Cloning and functional studies of a luxO regulator LuxT from Vibrio
 RT harveyi.";
 RL Biochim. Biophys. Acta 0:0-0(2001).
 DR EMBL: AF321123; AAK09362.1; -

SO SEQUENCE 153 AA; 17475 MW; 33837BB1A2A1819B CRC64;

Query Match 69.2%; Score 18; DB 2; Length 153;

Best Local Similarity 40.0%; Pred. No. 34;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXXLD 10

DB 54 KKTDFETALD 63

RESULT 10

Q8MUVS PRELIMINARY; PRT; 160 AA.

AC Q8MUVS; 08MUVS; 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SKIN;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC019336; AAL19336.1; -

KW Hypothetical protein.

FT NON_TER 1

SO SEQUENCE 160 AA; 17041 MW; 9F7B497AAC06EDB8 CRC64;

Query Match 69.2%; Score 18; DB 4; Length 160;

Best Local Similarity 40.0%; Pred. No. 35;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXXLD 10

DB 52 KKSAAESMID 61

RESULT 11

Q9KLJ2 PRELIMINARY; PRT; 161 AA.

AC Q9KLJ2; 09KLJ2; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

OS Transcriptional regulator, TetR family.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N16961 / SEROTYPE O1;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,

RA Gill S.R., Nelson K.E., Read T.D., Jettelin H., Richardson D.,

RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

RA McDonald L., Utterback T., Fleischmann R.D., Nieman W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio

RT cholerae."

RL Nature 406:477-483(2000).

DR EMBL: AE004419; AAF96814.1; -

DR TIGR: AC0917; -

KW Complete proteome.

SO SEQUENCE 161 AA; 18749 MW; AA78003D18984288 CRC64;

Query Match 69.2%; Score 18; DB 16; Length 161;

Best Local Similarity 40.0%; Pred. No. 35;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXXLD 10

DB 62 KKTDFASALD 71

RESULT 12

O04541 PRELIMINARY; PRT; 171 AA.

AC O04541; 004541; 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC Euphorbia; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Osborn B.I., Vysotskaya V.S., Toriumi M., Yu G., Oji O., Buehler E.,

RA Conway A.B., Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,

RA Shin F., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,

RA Theologis A.;

RT "The sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1.";

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Theologis A.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC002062; AAB61109.1; -

DR InterPro: IPR003822; PAH.

DR Pfam: PF02671; PAH; 2.

SO SEQUENCE 171 AA; 19992 MW; 691285E59734CA73 CRC64;

Query Match 69.2%; Score 18; DB 10; Length 171;

Best Local Similarity 40.0%; Pred. No. 37;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KKKXXXXXXLD 10

DB 16 KLTFTTALD 25

RESULT 13

Q9D8S4 PRELIMINARY; PRT; 205 AA.

AC Q9D8S4; 09D8S4; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 1810038D15R1k protein (RIKEN CDNA 1810038D15 gene).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Koenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schenl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boiffell D., Bojunga N., Carrinci P., de Ronaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamilya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaez P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007731; BAB25219.1; -;
 DR EMBL; BC003445; AAH03445.1; -;
 DR MGD; MGI:1916430; 1810038D15Rik.
 DR InterPro; IPR000520; Exonuclease.
 DR Pfam; PF00929; Exonuclease; 1.
 DR SMART; SM00479; EXOIII; 1.
 SQ SEQUENCE 205 AA; 23613 MW; D3FF9C7014B730E CRC64;
 Query Match 69.2%; Score 18; DB 11; Length 205;
 Best Local Similarity 40.0%; Pred. No. 43;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 KKKXXXXXXD 10
 Db 157 KKAASHRALD 166
 RESULT 14
 ID 08X427 PRELIMINARY; PRT; 212 AA.
 AC 08X427;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative tet operon regulator.
 GN YCDC OR 21512 OR ECS1259.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 NCBI_TaxID=83334;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-O157:H7 / EDL933 / ATCC 700927;
 RC MEDLINE-21074935; PubMed-11206551;
 RA Berra N.T., Plunkett G., Iii, Burland V., Mau B., Glasner J.D.,
 RA Rose D.V., Maynew G.F., Evans P.S., Gregor J., Kiripatrick H.A.,
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimailanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blatter F.R.;
 RT Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.*;
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / RIMD 0509952;
 RM MEDLINE-21156231; PubMed-11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shida T., Hattori M., Shingawa H.;
 RT Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.*;
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AE005301; AAG55629.1; -;

DR EMBL; AP002554; BAB34682.1; -;
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; tetr; 1.
 DR PRINTS; PR00445; HHTETR.
 KW Complete proteome.
 SQ SEQUENCE 212 AA; 23703 MW; 5DA47B85C960F0DC CRC64;
 Query Match 69.2%; Score 18; DB 16; Length 212;
 Best Local Similarity 40.0%; Pred. No. 45;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 KKKXXXXXXD 10
 Db 20 KKAALSALD 29
 RESULT 15
 ID 096609 PRELIMINARY; PRT; 215 AA.
 AC 096609;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Surface antigen ariel1.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-HM1-TMSS;
 RC MEDLINE-98084495; PubMed-9423879;
 RA Mai Z., Samuelson J.;
 RT "A new gene family (ariel) encodes asparagine-rich Entamoeba
 RT histolytica antigens, which resemble the amebic vaccine candidate
 RT serine-rich E. histolytica protein.*;
 RL Infect. Immun. 66:353-355(1998).
 DR EMBL; AF093575; AAC72364.1; -;
 SQ SEQUENCE 215 AA; 23641 MW; 00B59B87816A5ECD CRC64;
 Query Match 69.2%; Score 18; DB 5; Length 215;
 Best Local Similarity 40.0%; Pred. No. 45;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 KKKXXXXXXD 10
 Db 50 KKSSNSSELD 59
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 Job time : 32.0909 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:47:43 ; Search time 33.9394 Seconds
(without alignments)
39.261 Million cell updates/sec

Title: US-09-150-947F-15

Perfect score: 15
Sequence: 1 xxxxxxxxxd 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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23: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	2	2	AA10185
2	6	40.0	2	21	AA10185
3	6	40.0	3	5	AA10185
4	6	40.0	3	11	AA10185
5	6	40.0	3	13	AA10185
6	6	40.0	3	13	AA10185
7	6	40.0	3	14	AA10185
8	6	40.0	3	14	AA10185
9	6	40.0	3	14	AA10185
10	6	40.0	3	14	AA10185

11	6	40.0	3	15	AA10185
12	6	40.0	3	15	AA10185
13	6	40.0	3	16	AA10185
14	6	40.0	3	16	AA10185
15	6	40.0	3	16	AA10185
16	6	40.0	3	16	AA10185
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18	6	40.0	3	17	AA10185
19	6	40.0	3	17	AA10185
20	6	40.0	3	17	AA10185
21	6	40.0	3	18	AA10185
22	6	40.0	3	18	AA10185
23	6	40.0	3	18	AA10185
24	6	40.0	3	18	AA10185
25	6	40.0	3	18	AA10185
26	6	40.0	3	19	AA10185
27	6	40.0	3	19	AA10185
28	6	40.0	3	19	AA10185
29	6	40.0	3	19	AA10185
30	6	40.0	3	19	AA10185
31	6	40.0	3	19	AA10185
32	6	40.0	3	19	AA10185
33	6	40.0	3	20	AA10185
34	6	40.0	3	20	AA10185
35	6	40.0	3	20	AA10185
36	6	40.0	3	20	AA10185
37	6	40.0	3	20	AA10185
38	6	40.0	3	20	AA10185
39	6	40.0	3	20	AA10185
40	6	40.0	3	20	AA10185
41	6	40.0	3	20	AA10185
42	6	40.0	3	20	AA10185
43	6	40.0	3	20	AA10185
44	6	40.0	3	21	AA10185
45	6	40.0	3	21	AA10185

ALIGNMENTS

RESULT 1	AA10185
ID	AA10185 standard; Protein; 2 AA.
XX	AA10185;
AC	16-ANG-2002 (updated)
DT	14-ANG-1992 (first entry)
XX	
DE	Sequence of synthetic polypeptide for the prodn. of aspartame.
KW	Aspartyl-phenylalanine methyl ester; artificial sweetener;
XX	aspartame.
OS	Synthetic.
XX	
PN	EP36258-A.
XX	
PD	23-SEP-1981.
XX	
PF	02-MAR-1981; 81EP-0300857.
XX	
PR	14-MAR-1980; 80US-0130462.
PA	(CETU-) CETUS CORP.
XX	
PI	Rose JE, White TV, Bahl CP;
XX	
DR	WPI; 1981-72133D/40.
XX	
PT	N-PDSB; AAN10059.
XX	
PT	Aspartame prodn. from synthetic polypeptide - produced by cloned microorganism

Platelet aggregati
N4-3 truncated GA
Non-RBD, non-YISGR
Cancer metastasis
RF-1 peptide 1 fro
HPR3 peptide deriv
Platelet-targetin
Active domain from
Mutant chemokine a
Human IL-16 5' end
Platelet-targeting
LDV-peptide capabl
RBD-peptide capabl
Angiotensin II pep
Peptide A1(1-3) u
Integrin receptor
Anti-inflammatory
Anti-inflammatory
Anti-inflammatory
Anti-inflammatory
Resin bound cyclic
Linker for dual av
Linker for dual av
Asparaginyl endope
Amino acid sequenc
Fibronectin protei
Fibronectin protei
RBD peptide. Unid
Peptide used in th
Trypsin modulating
Trypsin modulating

XX PS Disclosure; Page 5; 18pp; English.
CC CC The inventors claim a method for the prodn. of aspartame by first
CC synthesizing double-stranded DNA in which a coding strand has
CC alternating codons for Asp and the phe in sufficient number to
CC produce a polypeptide which is stable in predetermined host
CC microorganisms. The DNA strand is then inserted into a cloning
CC vehicle so that the resulting chimera directs the synthesis of the
CC Asp-Phe protein. This protein is then cleaved with CNBr or trypsin
CC by digestion with chymotrypsin.
CC (Updated on 16-AUG-2002 to add missing OS field.)
CC XX
SQ Sequence 2 AA;
Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 D 10
DB 1 D 1
RESULT 2
AAB37936
ID AAB37936 standard; peptide; 2 AA.
XX AC AAB37936;
XX DT 27-FEB-2001 (first entry)
XX DE Trypsin modulating oostatic factor (TMOF) peptide SEQ ID 41.
XX KM Trypsin modulating oostatic factor; TMOF, pesticide; pest control;
XX KW digestive enzyme synthesis inhibition; mosquito larvae; coleoptera;
XX KW lepidopteran; dipteran; blood-sucking insect; Diptera; Nematocera;
XX KW Colicidae; Culicinae; Corethrinae; Ceratopogonidae; Simuliidae.
XX OS Synthetic.
XX PM WO200063233-A2.
XX PD 26-OCT-2000.
XX PF 18-APR-2000; 2000WO-US10235.
XX PR 21-APR-1999; 99US-0295996.
XX PA (UYFL) UNIV FLORIDA RES FOUND INC.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Borovsky D, Linderman RJ;
XX DR WPI: 2000-687156/67.
XX PT Novel trypsin modulating oostatic factor compound peptides, useful for
XX PT pest control including pests of agricultural crops -
XX PS Claim 3; Page 33; 50pp; English.
XX This invention relates to a trypsin modulating oostatic factor (TMOF)
CC compound. The compound specifically does not include the TMOF analogue
CC peptides represented by AAB37942 - AAB37949. Sequences AAB37900 -
CC AAB37941 are TMOF analogues which may be included in the composition. The
CC TMOF compound has pesticidal activity and is an inhibitor of pest
CC digestive enzyme synthesis. The TMOF compound is useful for controlling
CC pests such as mosquito larvae, coleopterans, lepidopterans, dipterans or
CC blood-sucking insects of order Diptera, suborder Nematocera, family
CC Colicidae or subfamily Culicinae, Corethrinae, Ceratopogonidae and
CC Simuliidae.

SQ Sequence 2 AA;
Query Match 40.0%; Score 6; DB 21; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 D 10
DB 2 D 2
RESULT 3
AAP40819
ID AAP40819 standard; peptide; 3 AA.
XX AC AAP40819;
XX DT 03-AUG-1992 (first entry)
XX DE Sequence of fragment D corresp. to residues 25-27 of human
XX DE pancreatic growth hormone releasing factor (somatotrinin) (hpgRF).
XX KM Hormone; dwarfism; therapy; retarded growth;
XX KW anabolic protein deficiency; growth promoter; lactation.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Modified-site 1 /label= Boc-D(OBz1)
FT /note= "Boc-tertlobutylloxycarbonyl (carbamate);
FT OBz1-ester benzyllyque"
FT Modified-site 3 /label= M-NH-NH2
XX PM AU8424774-A.
XX PD 30-AUG-1984.
XX PF 20-FEB-1984; 84AU-0400343.
XX PR 29-NOV-1983; 83FR-0019058.
XX PR 21-FEB-1983; 83FR-0002781.
XX PA (SNFI) SANOFI SA.
XX PI Diaz J, Demarne H, Roncucci R, Schmelck PH;
XX DR WPI: 1984-256760/42.
XX PT Synthesis of hpgRF in liquid phase reactions - with use of new
XX PT peptide fragments
XX PS Claim 4; Page 67; 76pp; French.
XX The inventors claim hpgRF fragments used for the synthesis of hpgRF.
CC using the method somatotrinin can be obt. on a large scale with
CC good yield and good purity. The prod. is used in man for the
CC treatment of dwarfism and retarded growth and for anabolic protein
CC deficiencies. In animals it is useful for promoting wt. growth for
CC increased prodn., lactation etc. This index is based on Ep-122818,
CC which is the equivalent of AU8424774.
XX SQ Sequence 3 AA;
Query Match 40.0%; Score 6; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 D 10
DB 1 D 1

```

RESULT 4
AAR04607
ID AAR04607 standard; peptide; 3 AA.
XX
AC AAR04607;
XX
DT 05-SEP-1990 (first entry)
XX
DE Antiviral agent.
XX
KM Antiviral; M2; poliovirus; polio; hepatitis.
XX
OS Synthetic.
XX
PN JP02078631-A.
XX
PD 19-MAR-1990.
XX
PF 14-SEP-1988; 88JP-0228843.
XX
PR 14-SEP-1988; 88JP-0228843.
XX
PA (NIRA ) NIPPON MINING KK.
XX
DR WPI; 1990-129060/17.
XX
PT Antiviral agent contg. tri:peptide (unit) -
PT of basic aminoacid, then alanine, glycine or sarcosine, and
PT acidic aminoacid, effective against virus with protein-terminated DNA
or RNA.
XX
PS Disclosure; ; 4pp; Japanese.
XX
CC Peptide is effective against inhibiting propagation of DNA or RNA
CC bonded, protein containing viruses eg. Poliovirus, Hepatitis virus.
XX
SQ Sequence 3 AA;

Query Match          40.0%; Score 6; DB 11; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      10 D 10
      1
      3 D 3
Db

RESULT 5
AAR00718
ID AAR00718 standard; peptide; 3 AA.
XX
AC AAR00718;
XX
DT 29-MAY-1990 (first entry)
XX
DE Core repeat of cell-adhesive protein.
XX
KM Cell adhesion; anti-metastatic agent; immunomodulation; core repeat.
XX
PN EP347931-A.
XX
PD 27-DEC-1989.
XX
PF 23-JUN-1989; 89EP-0111468.
XX
PR 24-JUN-1988; 88JP-0156133.
XX
PA (AZUMA/) AZUMA I.
XX
PI Sakai I, Nishi N, Azuma I, Tokura S;
XX
DR WPI; 1990-001305/01.

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XX
XX Polypeptide with repeated sequences of cell adhesion protein used
PT as anti-metastatic agent for cancer and agonist or antagonist of
PT cell-adhesion proteins
XX
PS Claim 2; page 14; 16pp; English.
XX
CC Peptide core is repeated 2-20 times to form a cell-adhesive protein of
CC mol. wt. 1,500-5,000. The protein is an (ant)agonist of cell-adhesive
CC proteins such as fibronectin. It has high antimetastatic activity
CC against cancer and can be used in immunomodulation, wound healing,
CC platelet aggregation inhibition and alleviation of neuro-disorders.
CC See also AAR00722.
XX
SQ Sequence 3 AA;

Query Match          40.0%; Score 6; DB 11; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      10 D 10
      1
      3 D 3
Db

RESULT 6
AAR25615
ID AAR25615 standard; peptide; 3 AA.
XX
AC AAR25615;
XX
DT 20-JAN-1993 (first entry)
XX
DE Harvey Ras inhibitor - Ras 30-32.
XX
KM GTPase; activating protein; GAP; oncogenesis; cancer; truncated;
KM colorectal; exocrine pancreatic; myeloid leukaemia; adenyl acylase.
XX
OS Synthetic.
XX
PN EP496162-A.
XX
PD 29-JUL-1992.
XX
PF 16-DEC-1991; 91EP-0311658.
XX
PR 24-DEC-1990; 90US-0632891.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Freidinger RM, Garsky VM, Gibbs JB, Schaber MD, Sigal IS;
XX
DR WPI; 1992-251427/31.
XX
PT Synthetic peptide inhibitors of Ras-GAP interaction - as
PT antitumour agents against e.g. colorectal carcinoma, exocrine
PT pancreatic carcinoma and myeloid leukaemia
XX
PS Claim 3; page 7; 31pp; English.
XX
CC The peptide corresponds to a C- and N-terminal truncated version of
CC the prod. of the Harvey ras oncogene from residues 17-44, i.e. from
CC residues 30-32. The peptide is capable of binding to GTPase
CC activating protein (GAP) thus inhibiting Ras activation by GAP and
CC inhibiting Ras-dependent cell transformation. Derivs. of the Ras
CC peptide are also provided, comprising C-terminal truncations, N-
CC terminal truncations, or modifications of specific amino acids, e.g.
CC the most potent Ras inhibitor is Ras 17-32. Oncogenic forms of Ras
CC occur in various human cancers, e.g. colorectal carcinoma, exocrine
CC pancreatic carcinoma and myeloid leukaemias. Ras complexed with GTP
CC can bind GAP and this is thought to be the important step in the
CC transformation activity of Ras. The peptide is also capable of
CC inhibiting GAP as well as the interaction of Ras with yeast

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CC adenylyl acylase. See also AAR25602-29.
 XX
 SQ Sequence 3 AA;

Query Match 40.0%; Score 6; DB 13; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 |
 Db 1 D 1

RESULT 7
 AAR36707
 ID AAR36707 standard; peptide: 3 AA.
 XX
 AC AAR36707;

XX 26-AUG-1993 (first entry)

DE Adhesion formation prevention RGD-contg. peptide.

XX Tissue repair; peritoneum; surgery; post-surgically; inhibition;
 KW platelet aggregation; cardiovascular; orthopedic; thoracic;
 KW ophthalmic; CNS; use.

XX Synthetic.

XX WO9308818-A.

XX 13-MAY-1993.

XX 06-NOV-1992; 92WO-US09494.

XX 07-NOV-1991; 91US-0789231.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega GS, Rodgers KE;

XX WPI; 1993-167381/20.

XX Prevention of adhesion formation, partic. post-surgically - comprises
 PT administering a RGD-contg. peptide for a time sufficient to permit
 PT tissue repair

PS Example; Page 18; 22pp; English.

XX The sequence is that of an RGD-contg. peptide which is used in a
 CC method for prevention of adhesion formation for a time sufficient
 CC to permit tissue repair. The method is used for minimizing or
 CC preventing adhesion formation, partic. in the peritoneum following
 CC surgery, but also for e.g. cardiovascular, orthopedic, thoracic,
 CC ophthalmic, CNS and other uses. In addn., the peptide inhibits
 CC platelet aggregation and does not induce inflammation or trauma
 CC at the site of administration.

XX Sequence 3 AA;

Query Match 40.0%; Score 6; DB 14; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 |
 Db 3 D 3

RESULT 8
 AAR30728
 ID AAR30728 standard; peptide: 3 AA.
 XX

AC AAR30728;
 XX
 DT 20-MAY-1993 (first entry)

DE IGE-mast cell reaction preventing peptide intermediate.

XX Basophil; protective group; fragment condensing.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-t-butoxycarbonyl-beta-benzyl-L-aspartyl"
 FT

XX JP04360898-A.

XX 14-DEC-1992.

XX 04-JUN-1991; 91JP-0159394.

XX 04-JUN-1991; 91JP-0159394.

XX (TANA) TANABE SEIYAKU CO.

XX WPI; 1993-032710/04.

XX L-Aspartyl-L-seryl-L-aspartyl-L-prolyl-L-arginine prepn. -
 PT involves fragment-condensing tri-peptide with amino-protected
 PT di-peptide to form penta-peptide
 XX Claim 7; Page 2; 8pp; Japanese.

XX The prepn. of DSDPR is claimed and involves e.g. fragment-condensing
 CC C-protected tripeptide with N-protected dipeptide to form pentapeptide
 CC and then removing the protective gps.
 CC N-t-butoxycarbonyl-beta-benzyl-L-aspartyl-L-prolyl-L-arginine is a
 CC new cpd."

XX Sequence 3 AA;

Query Match 40.0%; Score 6; DB 14; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 |
 Db 1 D 1

RESULT 9
 AAR30753
 ID AAR30753 standard; peptide: 3 AA.
 XX

XX AAR30753;

XX 26-MAY-1993 (first entry)

XX IGE-mast cell reaction inhibitory peptide prepn. peptide.

XX Physiologically active; basophil; tripeptide.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-t-butoxycarbonyl-beta-benzyl-L-Asp"
 FT Modified-site 5 /note= "N(G)-nitro-L-Arg benzyl ester"
 FT

XX JP04360899-A.

XX 14-DEC-1992.

PF 04-JUN-1991; 91JP-0159492.
 XX
 PR 04-JUN-1991; 91JP-0159492.
 XX
 PA (TANA) TANABE SEIYAKU CO.
 XX
 DR WPI; 1993-032711/04.
 XX
 PT Prepn. of physiologically active penta-peptide - comprises fragment-
 PT condensing specified carboxyl protected tri-peptide and amino-
 PT protected di-peptide and removing protective gps.
 XX
 PS Claim; Page 2; 8pp; Japanese.
 XX
 CC The peptide is used in the prepn. (claimed) of a physiologically.
 CC active and prevents the Ige - mast cell (basophil) reaction.
 XX
 SQ Sequence 3 AA;

Query Match 40.0%; Score 6; DB 14; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 1 D 1

RESULT 10
 AAR53144
 ID AAR53144 standard; peptide; 3 AA.
 XX
 AC AAR53144;
 XX
 DT 02-JUN-1994 (first entry)
 XX
 DE RGD peptide derivative #6.
 XX
 KW Drug; organ transplantation; rejection; immune disorder;
 KW systemic lupus.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "C9H19CO-Arg, C13H27CO-Arg, C15H31CO-Arg,
 FT CH3-[(CH(CH3))- (CH2)3]3-CH(CH3)-CH2-CO-Arg or
 FT CH3-[(CH(CH3))- (CH2)3]2-CH(CH3)-CH2-CO-Arg"
 FT Modified-site 4 /note= "Asp-OH or Asp-NH2"
 FT
 FT
 PN JP05255105-A.
 XX
 PD 05-OCT-1993.
 XX
 PF 16-MAR-1992; 92JP-0058460.
 XX
 PR 16-MAR-1992; 92JP-0058460.
 XX
 PA (FUJI) FUJI PHOTO FILM CO LTD.
 XX
 DR WPI; 1993-348360/44.
 XX
 PT Immuno-control drug for organ transplant rejection etc. - contains
 PT peptide having arginine, glycine, aspartic acid sequence
 XX
 PS Disclosure; Page 3; 11pp; Japanese.
 XX
 CC The sequences given in AAR44043-47 and AAR53144 represent examples of
 CC the claimed RGD containing peptide of the invention. These peptides all
 CC correspond to the generic formulae:
 CC HO2-(CH2)m-C(O)-[(X)-Arg-Gly-Asp-(Y)]n-O-CH2CH(OR1)CH2OR2 or
 CC R3-[(X)-Arg-Gly-Asp-(Y)]n-Z

CC [X], [Y] = amino acid or peptide residues;
 CC m = 1-5;
 CC n = 1-5;
 CC R1, R2 = H or 8-24C acyl or alkyl;
 CC R3 = 6-24C acyl;
 CC Z = hydroxyl or amino.
 CC These peptides form the active part of drugs which are used for the
 CC control of organ transplantation rejection or immune disorders such
 CC as systemic lupus.
 XX
 SQ Sequence 3 AA;

Query Match 40.0%; Score 6; DB 14; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 3 D 3

RESULT 11
 AAR44666
 ID AAR44666 standard; peptide; 3 AA.
 XX
 AC AAR44666;
 XX
 DT 20-JAN-1995 (first entry)
 XX
 DE Platelet aggregation or adhesion inhibitor - peptide 5.
 XX
 KW Platelet aggregation; adhesion; inhibitor; quest; host;
 KW beta-cyclodextrin; protease; resistance; degradation.
 XX
 OS Synthetic.
 XX
 PN JP06116289-A.
 XX
 PD 26-APR-1994.
 XX
 PF 09-OCT-1992; 92JP-0271294.
 XX
 PR 09-OCT-1992; 92JP-0271294.
 XX
 PA (FUJI) FUJI PHOTO FILM CO LTD.
 XX
 DR WPI; 1994-173759/21.
 XX
 PT Complex of adhesion peptide in host molecule e.g.
 PT beta-cyclodextrin - useful as platelet aggregation inhibitor
 PT which is resistant to protease degradation in-vivo
 XX
 PS Disclosure; Page 4; 5pp; Japanese.
 XX
 CC A peptide complex contg. peptide 5 as guest mol. is useful as a
 CC platelet aggregation or adhesion inhibitor. It is hardly hydrolysed
 CC by protease in vivo and thus maintains its effect for a long period.
 XX
 SQ Sequence 3 AA;

Query Match 40.0%; Score 6; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 3 D 3

RESULT 12
 AAR48960
 ID AAR48960 standard; Protein; 3 AA.
 XX

AC AAR48960;
 XX 12-SEP-1994 (first entry)
 DT
 XX
 DE NL4-3 truncated GAG C-terminal peptide.
 XX
 XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
 KM naturally occurring virus; NOV; translation; replication; infectivity;
 KM hepatitis B; HIV-2; SIV; flip-over PCR.
 XX
 OS Synthetic.
 XX
 PN WO9403596-A.
 XX 17-FEB-1994.
 PD
 XX 30-JUL-1993; 93WO-US07179.
 PF
 XX 30-JUL-1992; 92US-0921104.
 PR
 XX (UYHA-) UNIV HAWAII.
 PA
 XX Hu W, Wang J;
 PI
 XX WPI: 1994-065685/08.
 DR N-PSDB; AA057688.
 XX
 XX New antisense viruses and anti-sense-ribozyme viruses - used for
 PT treating or preventing viral infections, partic. HIV-1, HIV-2 or
 PT SIV infection
 PS
 PS Disclosure: Page 108; 167pp; English.
 XX
 CC This sequence is encoded by a PCR fragment of NL4-3 and represents the
 CC C-terminal peptide fragment of the truncated GAG protein. The DNA
 CC encoding this fragment was ligated into ClaI/SalI digested pX and the
 CC corresponding plasmid was used to produce the antisense virus of the
 CC invention. Antisense or truncated RNAs expressed by these viruses
 CC bind to the mRNAs expressed by the naturally occurring viruses (NOVs)
 CC and prevent the mRNAs from being translated into proteins, thereby
 CC preventing the NOV from replicating. The antisense viruses maintain
 CC the infectivity of the NOVs, allowing antisense RNAs to reach the
 CC mRNAs of the natural viruses. Antisense viruses such as these may be
 CC used for treating or preventing a viral infection, particularly HIV-1,
 CC HIV-2 or SIV infection or hepatitis B infection.
 CC
 SQ Sequence 3 AA;
 Query Match 40.0%; Score 6; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 |
 Db 2 D 2

RESULT 13
 AAR82907
 ID AAR82907 standard; peptide: 3 AA.
 XX
 AC AAR82907;
 XX
 DT 20-DEC-1995 (first entry)
 XX
 DE Non-RGD, non-YISGR cancer metastasis inhibitory peptide #1.
 XX
 KW Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;
 KW water soluble polysaccharide; metastasis; wound; immunogenicity.
 XX
 OS Synthetic.
 XX
 PN JP07089999-A.

XX 04-APR-1995.
 PD
 XX 17-SEP-1993; 93JP-0254779.
 PF
 XX 17-SEP-1993; 93JP-0254779.
 PR
 XX (JABG) NIPPON ZEON KK.
 PA
 XX WPI: 1995-167254/22.
 DR
 XX
 PT Cancer metastasis inhibitive peptide derivs. - useful for inhibition
 PT of cancer metastasis, healing of wounds and regulation of
 PT immunogenicity.
 PS
 PS Disclosure: Page 3; 6pp; Japanese.
 CC
 CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
 CC inhibit cancer metastasis. They are composed of an adhesive peptide
 CC with a core sequence selected from: RGD (AAR70472-85), YIGSR
 CC (AAR70486-90) or other sequence (AAR82907-24), linked to a water soluble
 CC polysaccharide, preferably a water soluble dextran, at the C-terminus.
 CC The peptides are useful in inhibiting cancer metastasis, healing wounds
 CC and the regulation of immunogenicity.
 CC
 SQ Sequence 3 AA;
 Query Match 40.0%; Score 6; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 |
 Db 2 D 2

RESULT 14
 AAR70472
 ID AAR70472 standard; peptide: 3 AA.
 XX
 AC AAR70472;
 XX
 DT 20-DEC-1995 (first entry)
 XX
 DE Cancer metastasis inhibitory peptide core RGD sequence.
 XX
 KW Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;
 KW water soluble polysaccharide; metastasis; wound; immunogenicity.
 XX
 OS Synthetic.
 XX
 PN JP07089999-A.
 XX
 PD 04-APR-1995.
 PF
 XX 17-SEP-1993; 93JP-0254779.
 PF
 XX 17-SEP-1993; 93JP-0254779.
 PR
 XX (JABG) NIPPON ZEON KK.
 PA
 XX WPI: 1995-167254/22.
 DR
 XX
 PT Cancer metastasis inhibitive peptide derivs. - useful for inhibition
 PT of cancer metastasis, healing of wounds and regulation of
 PT immunogenicity.
 PS
 PS Disclosure: Page 2; 6pp; Japanese.
 CC
 CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
 CC inhibit cancer metastasis. They are composed of an adhesive peptide
 CC with a core sequence selected from: RGD (AAR70472-85), YIGSR
 CC (AAR70486-90) or other sequence (AAR82907-24), linked to a water soluble
 CC polysaccharide, preferably a water soluble dextran, at the C-terminus.
 CC The peptides are useful in inhibiting cancer metastasis, healing wounds
 CC and the regulation of immunogenicity.

CC polysaccharide, preferably a water soluble dextran, at the C-terminus.
 CC The peptides are useful in inhibiting cancer metastasis, healing wounds
 CC and the regulation of immunogenicity.

XX Sequence 3 AA;

Query Match 40.0%; Score 6; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10

DB 3 D 3

RESULT 15

ID AAR64556 standard; Peptide; 3 AA.

AC AAR64556;

DT 01-SEP-1995 (first entry)

DE RF-1 peptide 1 from respiratory syncytial virus.

KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41;

KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;

RSV.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1 /note="optionally has an amino, acetyl,

FT 9-fluorenylmethoxy-carbonyl, hydrophobic or

macromolecular carrier gp. attached"

FT Modified-site 3 /note="optionally has a carboxyl, amido, hydrophobic

or macromolecular carrier gp. attached"

XX WO9428920-A.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US05739.

XX 07-JUN-1993; 93US-0073028.

XX (UYDU-) UNIV DUKE.

PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;

PI Petteway SR, Wild CT;

XX WPI; 1995-036105/05.

DR Computer search generated synthetic peptides - are inhibitors of

PT HIV transmission

XX Claim 14; Page 137; 182pp; English.

XX AAR64556-589 are peptide derivatives of a 37 mer RF-1 peptide derived

CC from respiratory syncytial virus (RSV) (AAR64590) which have been

CC truncated at the carboxy terminus. The peptides are DP-178 like

CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1

CC isolate LAI transmembrane protein gp41. It forms a putative alpha

CC helix at the C-terminal end of the gp41 ectodomain, and complexes

CC with DP-107 (corresponds to amino acids 558-595) which contains a

CC leucine zipper motif. The peptides complex via non-covalent

CC protein-protein interactions. The peptide derivatives were

CC identified by a computer assisted peptide sequence search. The

CC antiviral activity of this peptide is not stated in the

CC specification.

XX Sequence 3 AA;

Query Match 40.0%; Score 6; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10

DB 3 D 3

Search completed: June 5, 2003, 16:00:25
 Job time : 35.9394 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2003, 15:23:33 ; Search time 8.78788 Seconds
(without alignments)
33.481 Million cell updates/sec

Title: US-09-150-947F-15

Perfect score: 15

Sequence: 1 XXXXXXXXXXD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	40.0	2	1	US-07-820-154A-15
2	6	40.0	2	1	US-07-820-154A-23
3	6	40.0	2	1	US-07-820-154A-33
4	6	40.0	2	1	US-07-820-154A-39
5	6	40.0	2	1	US-08-358-150-171
6	6	40.0	2	1	US-08-153-799-20
7	6	40.0	2	2	US-08-097-554A-15
8	6	40.0	2	2	US-08-097-554A-23
9	6	40.0	2	2	US-08-097-554A-33
10	6	40.0	2	2	US-08-097-554A-39
11	6	40.0	2	2	US-08-539-433-15
12	6	40.0	2	2	US-08-539-433-16
13	6	40.0	2	2	US-08-539-433-17
14	6	40.0	2	2	US-09-327-424-2
15	6	40.0	2	3	US-08-480-640A-15
16	6	40.0	2	3	US-08-480-640A-23
17	6	40.0	2	3	US-08-480-640A-33
18	6	40.0	2	3	US-08-480-640A-39
19	6	40.0	2	3	US-08-295-802-15
20	6	40.0	2	3	US-08-295-802-23
21	6	40.0	2	3	US-08-295-802-33
22	6	40.0	2	3	US-08-295-802-39
23	6	40.0	2	4	US-09-326-335-2
24	6	40.0	2	4	US-08-488-237A-15
25	6	40.0	2	4	US-08-488-237A-23
26	6	40.0	2	4	US-08-488-237A-33
27	6	40.0	2	4	US-08-488-237A-39

28	6	40.0	2	4	US-08-375-992A-15	Sequence 15, Appl
29	6	40.0	2	4	US-08-375-992A-23	Sequence 23, Appl
30	6	40.0	2	4	US-08-375-992A-33	Sequence 33, Appl
31	6	40.0	2	4	US-08-375-992A-39	Sequence 39, Appl
32	6	40.0	2	4	US-09-295-996B-15	Sequence 23, Appl
33	6	40.0	2	4	US-09-295-996B-23	Sequence 35, Appl
34	6	40.0	2	4	US-09-295-996B-33	Sequence 58, Appl
35	6	40.0	2	5	PCR-US93-00324-15	Sequence 15, Appl
36	6	40.0	2	5	PCR-US93-00324-23	Sequence 23, Appl
37	6	40.0	2	5	PCR-US93-00324-33	Sequence 33, Appl
38	6	40.0	2	5	PCR-US93-00324-39	Sequence 39, Appl
39	6	40.0	3	1	US-07-748-943-2	Sequence 2, Appl
40	6	40.0	3	1	US-07-780-790A-1	Sequence 1, Appl
41	6	40.0	3	1	US-08-169-524-6	Sequence 6, Appl
42	6	40.0	3	1	US-08-081-539-117	Sequence 117, App
43	6	40.0	3	1	US-08-251-027-1	Sequence 1, Appl
44	6	40.0	3	1	US-08-251-027-2	Sequence 2, Appl
45	6	40.0	3	1	US-08-251-027-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-07-820-154A-15
Sequence 15, Application US/07820154A
Patent No. 5382425

GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-15

Query Match 40.0% Score 6; DB 1; Length 2;
Best Local Similarity 100.0% Pred No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 1 D 1

RESULT 2
US-07-820-154A-23

Sequence 23, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820.154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-23

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 3
US-07-820-154A-33
Sequence 33, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820.154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-33

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 4
US-07-820-154A-39
Sequence 39, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820.154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-39

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 5
US-08-358-160-171
Sequence 171, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28, 005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-171

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 D 10
1 D 1

RESULT 6
US-08-153-799-20
Sequence 20, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J

APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-799-20

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 D 10
1 D 1

RESULT 7
US-08-097-554A-15
Sequence 15, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Syriepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-15

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 8
US-08-097-554A-23
Sequence 23, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-23

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 9
US-08-097-554A-33
Sequence 33, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-33

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 10
US-08-097-554A-39
Sequence 39, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-39

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 11
US-08-539-432-15
Sequence 15, Application US/08539432
Patent No. 5872210
GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: TRANSFRAME INHIBITORY
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
US-08-539-432-15

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 12
US-08-539-432-16
Sequence 16, Application US/08539432
Patent No. 5872210
GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: TRANSFRAME INHIBITORY
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
US-08-539-432-16

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 13
US-08-539-432-17
Sequence 17, Application US/08539432
Patent No. 5872210
GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: TRANSFRAME INHIBITORY
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10054

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
US-08-539-432-17

Query Match 40.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 14
US-09-327-424-2
Sequence 2, Application US/09327424
Patent No. 6027903
GENERAL INFORMATION:
APPLICANT: Eyre, David R
TITLE OF INVENTION: KIT FOR DETECTING ANALYTE INDICATIVE OF TYPE I COLLAGEN
TITLE OF INVENTION: RESORPTION IN VIVO (as amended)
FILE REFERENCE: WROS-1-14019
CURRENT APPLICATION NUMBER: US/09/327,424
CURRENT FILING DATE: 1993-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: N-telopeptide sequence of type II collagen
US-09-327-424-2

Query Match 40.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 2 D 2

RESULT 15
US-08-480-640A-15
Sequence 15, Application US/08480640A
Patent No. 6033904
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-640A-15

Query Match 40.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

Search completed: June 5, 2003, 15:32:43
Job time : 8.78788 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:01 ; Search time 12.1212 Seconds
(Without alignments)
85.173 Million cell updates/sec

Title: US-09-150-947f-15
Perfect score: 15
Sequence: 1 xxxxxxxxxxxx 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCOT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCOTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	2	9	US-10-187-339-6 Sequence 6, App1
2	6	40.0	2	9	US-10-206-699-296 Sequence 296, App
3	6	40.0	2	10	US-09-983-172-8 Sequence 8, App1
4	6	40.0	2	10	US-09-983-172-105 Sequence 105, App
5	6	40.0	3	9	US-09-900-936-11 Sequence 11, App1
6	6	40.0	3	9	US-09-840-277-31 Sequence 31, App1
7	6	40.0	3	9	US-09-747-408-21 Sequence 21, App1
8	6	40.0	3	9	US-10-014-162-37 Sequence 37, App1
9	6	40.0	3	9	US-10-039-876A-3 Sequence 3, App1
10	6	40.0	3	9	US-10-039-876A-4 Sequence 4, App1
11	6	40.0	3	9	US-10-015-979-58 Sequence 58, App1
12	6	40.0	3	9	US-10-226-956-316 Sequence 316, App
13	6	40.0	3	9	US-10-226-956-317 Sequence 317, App
14	6	40.0	3	9	US-10-226-956-318 Sequence 318, App
15	6	40.0	3	9	US-10-226-956-319 Sequence 319, App
16	6	40.0	3	9	US-10-128-198-1 Sequence 1, App1
17	6	40.0	3	9	US-10-237-850-81 Sequence 81, App1
18	6	40.0	3	9	US-10-032-818-6 Sequence 6, App1
19	6	40.0	3	9	US-10-281-652-11 Sequence 11, App1

20	6	40.0	3	9	US-10-283-838-13 Sequence 13, App1
21	6	40.0	3	9	US-10-163-587A-19 Sequence 19, App1
22	6	40.0	3	9	US-10-141-531-15 Sequence 15, App1
23	6	40.0	3	9	US-10-141-531-16 Sequence 16, App1
24	6	40.0	3	9	US-10-141-531-17 Sequence 17, App1
25	6	40.0	3	9	US-10-141-531-18 Sequence 18, App1
26	6	40.0	3	9	US-10-141-531-19 Sequence 19, App1
27	6	40.0	3	9	US-10-141-531-20 Sequence 20, App1
28	6	40.0	3	10	US-09-096-749A-113 Sequence 113, App
29	6	40.0	3	10	US-09-866-824A-9 Sequence 9, App1
30	6	40.0	3	10	US-09-792-200B-19 Sequence 19, App1
31	6	40.0	3	10	US-09-771-192-11 Sequence 11, App1
32	6	40.0	3	10	US-09-853-918-1 Sequence 1, App1
33	6	40.0	3	10	US-09-853-918-6 Sequence 6, App1
34	6	40.0	3	10	US-09-682-667-14 Sequence 14, App1
35	6	40.0	3	10	US-09-867-847-30 Sequence 30, App1
36	6	40.0	3	10	US-09-922-261-7 Sequence 7, App1
37	6	40.0	3	10	US-09-312-762A-12 Sequence 12, App1
38	6	40.0	3	10	US-09-982-172-184 Sequence 184, App
39	6	40.0	3	10	US-09-837-697A-11 Sequence 11, App1
40	6	40.0	3	12	US-10-003-674A-6 Sequence 6, App1
41	6	40.0	4	1	US-08-464-363-35 Sequence 35, App1
42	6	40.0	4	1	US-08-610-220A-2 Sequence 2, App1
43	6	40.0	4	1	US-08-610-220A-7 Sequence 7, App1
44	6	40.0	4	1	US-08-610-220A-8 Sequence 8, App1
45	6	40.0	4	8	US-08-765-244-16 Sequence 16, App1

ALIGNMENTS

RESULT 1
US-10-187-339-6
; Sequence 6, Application US/10187339
; Publication No. US20030084478A1
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/10/187,339
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/434,837
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,185
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-187-339-6

Query Match 40.0%; Score 6; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 3; 3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
DB 2 D 2

RESULT 2
US-10-206-699-296
; Sequence 296, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699

```

; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 296
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-296

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```

Query Match          40.0%; Score 6; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      10 D 10
DB      2 D 2

```

```

RESULT 3
US-09-982-172-8
; Sequence 8, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emli Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-8

```

```

Query Match          40.0%; Score 6; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      10 D 10
DB      1 D 1

```

```

RESULT 4
US-09-982-172-105
; Sequence 105, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emli Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 2

```

```

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-105

```

```

Query Match          40.0%; Score 6; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      10 D 10
DB      1 D 1

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RESULT 5
US-09-900-936-11
; Sequence 11, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: dizege, Kathleen
; APPLICANT: Rodgers, Kathleen
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-3)
US-09-900-936-11

```

```

Query Match          40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      10 D 10
DB      1 D 1

```

```

RESULT 6
US-09-840-277-31
; Sequence 31, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIRO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-31

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Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 10 D 10
DB 3 D 3

RESULT 7

US-09-747-408-21
; Sequence 21, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-21

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 10 D 10
DB 1 D 1

RESULT 8

US-10-014-162-37
; Sequence 37, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH/75,001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-37

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 10 D 10
DB 1 D 1

RESULT 9

US-10-039-876A-3
; Sequence 3, Application US/10039876A
; Publication No. US20030032792A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, 2219A
; FILE REFERENCE: 97-63C1
; CURRENT APPLICATION NUMBER: US/10/039,876A
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/061,712
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif 1, corresponding to residues 127 to 129 of
US-10-039-876A-3

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 10 D 10
DB 2 D 2

RESULT 10

US-10-039-876A-4
; Sequence 4, Application US/10039876A
; Publication No. US20030032792A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Hal
; TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, 2219A
; FILE REFERENCE: 97-63C1
; CURRENT APPLICATION NUMBER: US/10/039,876A
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/061,712
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: US 09/167,513
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif 2, corresponding to residues 156 to 158 of
US-10-039-876A-4

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 10 D 10
DB 2 D 2

RESULT 11

US-10-015-979-58
; Sequence 58, Application US/10015979
; Publication No. US20030036050A1

GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; APPLICANT: Verhaert, Raymond M.D.
; APPLICANT: Beekwilder, Martinus J.
; APPLICANT: Aehle, Wolfgang
; TITLE OF INVENTION: Enzyme Selection
; FILE REFERENCE: 2183-5207US
; CURRENT APPLICATION NUMBER: US/10/015,979
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/NL00/00399
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/138,443
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CB4 domain of mutant 13
; NAME/KEY: SITE
; LOCATION: (1)-(3)
; OTHER INFORMATION:
US-10-015-979-58

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
Db 3 D 3

RESULT 12
US-10-226-956-316
; Sequence 316, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshl, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 316
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-226-956-316

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
Db 1 D 1

RESULT 13
US-10-226-956-317

; Sequence 317, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshl, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 317
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-226-956-317

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
Db 1 D 1

RESULT 14
US-10-226-956-318
; Sequence 318, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshl, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 318
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-226-956-318

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
Db 1 D 1

RESULT 15
US-10-226-956-319
; Sequence 319, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:

APPLICANT: Brophy, Colleen
APPLICANT: Komalavilas, Padmini
APPLICANT: Panitch, Alyssa
APPLICANT: Joshi, Lokesh
APPLICANT: Seal, Brandon L.
TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
FILE REFERENCE: ASD-1061-US
CURRENT APPLICATION NUMBER: US/10/226,956
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/314,535
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn version 3.1
SEQ ID NO 319
LENGTH: 3
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-226-956-319

Query Match 40.0%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
1
Db 1 D 1

Search completed: June 5, 2003, 15:49:05
Job time : 14.1212 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:24:01 ; Search time 9.84848 Seconds
(without alignments)
97.613 Million cell updates/sec

Title: US-09-150-947f-15

Perfect score: 15

Sequence: 1 XXXXXXXXXXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	4	2 I40697	biotin A - Citroba
2	6	40.0	4	2 A41890	protein D - Escher
3	6	40.0	4	2 D41654	hypothetical prote
4	6	40.0	4	2 A32480	achatin-I - giant
5	6	40.0	4	2 I51049	metallochionein-A
6	6	40.0	4	2 PT0271	Ig heavy chain CRD
7	6	40.0	4	2 B53284	T-cell receptor be
8	6	40.0	4	2 PT0696	T-cell receptor be
9	6	40.0	4	2 PT0711	T-cell receptor be
10	6	40.0	4	2 A26209	protein-glutamine
11	6	40.0	5	2 A32516	cholecystokinin-5
12	6	40.0	5	2 C23751	spinal cord peptid
13	6	40.0	5	2 A26830	mitosis inhibiting
14	6	40.0	5	2 A32014	tram protein - Esc
15	6	40.0	5	2 B31836	20K protein - Rick
16	6	40.0	5	2 B60274	major protein anti
17	6	40.0	5	2 D60274	endo-1,4-beta-xyla
18	6	40.0	5	2 S70615	photosystem I 10.4
19	6	40.0	5	2 PQ0689	Ig heavy chain CRD
20	6	40.0	5	2 PT0267	Ig heavy chain CRD
21	6	40.0	5	2 PT0281	Ig heavy chain CRD
22	6	40.0	5	2 PT0308	Ig heavy chain CRD
23	6	40.0	5	2 PT0596	T-cell receptor be
24	6	40.0	5	2 PT0513	T-cell receptor be
25	6	40.0	5	2 PT0600	T-cell receptor be
26	6	40.0	5	2 PT0729	T-cell receptor be
27	6	40.0	5	2 PT0624	T-cell receptor be
28	6	40.0	5	2 PT0601	T-cell receptor be
29	6	40.0	5	2 PT0672	T-cell receptor be

30	6	40.0	5	2 PT0660	T-cell receptor be
31	6	40.0	5	2 PT0651	T-cell receptor be
32	6	40.0	5	2 PT0656	T-cell receptor be
33	6	40.0	5	2 PT0535	T-cell receptor be
34	6	40.0	5	2 PT0699	T-cell receptor be
35	6	40.0	5	2 PT0538	T-cell receptor be
36	6	40.0	5	2 PT0561	T-cell receptor be
37	6	40.0	5	2 PT0540	T-cell receptor be
38	6	40.0	5	2 PT0703	T-cell receptor be
39	6	40.0	5	2 PT0690	T-cell receptor be
40	6	40.0	5	2 PT0573	T-cell receptor be
41	6	40.0	5	2 PT0580	T-cell receptor be
42	6	40.0	5	2 PT0679	T-cell receptor be
43	6	40.0	5	2 S68326	blood cell protein
44	6	40.0	6	2 A61419	sarcosine dehydrog
45	6	40.0	6	2 B44510	hypothetical prote

ALIGNMENTS

RESULT 1
I40697
biotin A - Citrobacter freundii (fragment)
C/Species: Citrobacter freundii
C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C/Accession: I40697
R/Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A/Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citroba
A/Reference number: I40697; MID:89006280; PMID:2971595
A/Accession: I40697
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 14 <RES>
A/Cross-references: GB:M21922; MID:9144434

Query Match 40.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 3 D 3

RESULT 2

A41890
protein D - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C/Accession: A41890
R/Slettan, A.; Gebhardt, K.; Kristiansen, E.; Birreland, N.K.; Lindqvist, B.H.
J. Bacteriol. 174, 4094-4100, 1992
A/Title: Escherichia coli K-12 and B contain functional bacteriophage P2 ogr genes.
A/Reference number: A41890; MID:92283767; PMID:1597424
A/Accession: A41890
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-4 <SLE>
A/Cross-references: GB:M81463

Query Match 40.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 2 D 2

RESULT 3

D41654

hypothetical protein (sodc 5' region) - Haemophilus parainfluenzae (fragment)

C:Species: Haemophilus parainfluenzae

C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995

C:Accession: D41654

R:Kroll, J.S.; Langford, P.R.; Loynds, B.M.

J. Bacteriol. 173, 7449-7457, 1991

A:Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus parainfluenzae

A:Reference number: A1654; MUID:92041655; PMID:1936942

A:Accession: D41654

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-4 <KRO>

Query Match 40.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 4
A32480
A:Title: Achatin-I - giant African snail

N:Contains: Achatin-II

C:Species: Achatina fulica (giant African snail)

C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999

C:Accession: A32480

R:Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun

Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989

A:Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru

A:Reference number: A32480; MUID:89273551; PMID:2597281

A:Accession: A32480

A:Molecule type: Protein

A:Residues: 1-4 <RAM>

A>Note: stereochemistry of the active form confirmed by chemical synthesis

R:Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto

FEBS Lett. 307, 253-256, 1992

A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro

(H-Gly-Phe-Ala-Asp-OH).

A:Reference number: A44691; MUID:92354723; PMID:1644179

A:Contents: annotation: X-ray crystallography, 0.85 angstroms

A>Note: Achatin-II has L-phenylalanine

C:Keywords: D-amino acid

F:2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 40.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 4 D 4

RESULT 5
I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kiling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me

A:Reference number: I51049; MUID:95324545; PMID:7601121

A:Accession: I51049

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:91019799; PIDN:CA56466.1; PID:94379328

Query Match 40.0%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 2 D 2

RESULT 6
PT0271

Ig heavy chain CRD3 region (clone 3-103A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0271

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0271

A:Molecule type: DNA

A:Residues: 1-4 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 7
B53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: B53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity an

A:Reference number: A53284; MUID:91342695; PMID:1678859

A:Accession: B53284

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-4 <HAR>

A:Cross-references: GB:S60737; NID:9233916; PIDN:AB19518.1; PID:9233918

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)

C:Keywords: T-cell receptor

Query Match 40.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 8
PT0696

T-cell receptor beta chain V-D-J region (100-2N) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0696; PT0612; PT0545; PT0692; PT0552; PT0696

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0635

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-4 <FE2>
 A:Experimental source: newborn thymus, strain BALB/c, 100-2M
 A:Accession: PT0612
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE2>
 A:Experimental source: newborn thymus, strain BALB/c, 111-1J
 A:Accession: PT0545
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AD
 A:Accession: PT0692
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE4>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1M
 A:Accession: PT0552
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE5>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1CI
 A:Accession: PT0696
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE6>
 A:Experimental source: newborn thymus, strain BALB/c, 135-1AA
 C:Keywords: T-cell receptor

Query Match 40.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 4 D 4

RESULT 9

PT0711
 T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0607; PT0674; PT0570; PT0711; PT0710
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0607
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE1>
 A:Experimental source: newborn thymus, strain BALB/c, 120-2J
 A:Accession: PT0674
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE2>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
 A:Accession: PT0678
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
 A:Accession: PT0570
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE4>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
 A:Accession: PT0711
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE5>
 A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)

C:Keywords: T-cell receptor

Query Match 40.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 4 D 4

RESULT 10

A26209
 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 10-Sep-1987 #sequence_revision 10-Sep-1987 #text_change 03-Mar-1995
 C:Accession: A26209
 R:Connellan, J.M.; Chung, S.I.; Whetzel, N.K.; Bradley, L.M.; Folk, J.E.
 J. Biol. Chem. 246, 1093-1098, 1971
 A:Title: Structural properties of guinea pig liver transglutaminase.
 A:Reference number: A26209; MUID:7111415; PMID:5543674
 A:Accession: A26209
 A:Molecule type: protein
 A:Residues: 1-4 <CON>
 A:Experimental source: liver
 C:Keywords: aminoacyltransferase

Query Match 40.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 3 D 3

RESULT 11

A32516
 cholecystokinin-5 - dog
 N:Alternate names: CCK-5
 C:Species: Canis lupus familiaris (dog)
 C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
 C:Accession: A32516
 R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.
 Am. J. Physiol. 252, G272-G275, 1987
 A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
 A:Reference number: A32516; MUID:87153871; PMID:3826534
 A:Accession: A32516
 A:Molecule type: protein
 A:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; neuropeptide
 F/5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.0%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 4 D 4

RESULT 12

C23751
 spinal cord peptide SCP-6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 16-Aug-2000
 C:Accession: C23751
 R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou
 Arch. Biochem. Biophys. 240, 178-183, 1985
 A:Reference number: A23751; MUID:85250425; PMID:4015098

A:Accession: C23751
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 1-5 <HSI>
 C:Superfamily: unassigned animal peptides

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 5;
 Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 1 D 1

RESULT 13

A26830
 mitosis inhibiting peptide - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: A26830
 R:Reichelt, K.; Eljjo, K.; Edmanson, P.D.
 Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
 A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
 A:Reference number: A26830; MUID:87298602; PMID:3619940
 A:Accession: A26830
 A:Molecule type: Protein
 A:Residues: 1-5 <REI>
 C:Superfamily: unassigned animal peptides
 C:Keywords: blocked amino end; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 5;
 Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 3 D 3

RESULT 14

A32014
 trm protein - Escherichia coli plasmid R100 (fragment)
 C:Species: Escherichia coli
 C:Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
 C:Accession: A32014
 R:Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
 J. Bacteriol. 170, 2749-2757, 1988
 A:Title: Identification and characterization of the products from the trmJ and trmK genes
 A:Reference number: A32014; MUID:88227859; PMID:2836369
 A:Accession: A32014
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <TNA>
 C:Genetics:
 A:Genome: plasmid
 C:Keywords: DNA binding

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 5;
 Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 3 D 3

RESULT 15

B31836
 20K proteoln - Rickettsia rickettsii (fragment)
 C:Species: Rickettsia rickettsii
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999

C:Accession: B31836
 R:Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
 J. Bacteriol. 170, 4493-4500, 1988
 A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
 A:Reference number: A31836; MUID:89008059; PMID:3139629
 A:Accession: B31836
 A:Molecule type: DNA
 A:Residues: 1-5 <AND>
 A:Cross-references: GB:J03371; NID:9152455; PID:AA015030.1; PID:94262874

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 5;
 Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 2 D 2

Search completed: June 5, 2003, 15:34:00
 Job time : 10.8485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:34:07 ; Search time 6.5155 seconds

(without alignments)
63.661 Million cell updates/sec

Title: US-09-150-947F-15
Perfect score: 15
Sequence: 1 XXXXXXXXXXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	40.0	3	1	LUXE_VIBFI
2	6	40.0	4	1	ACH1_ACHFU
3	6	40.0	4	1	OCPI_OCTMI
4	6	40.0	4	1	OCPI_OCTMI
5	6	40.0	5	1	BIOA_CITFR
6	6	40.0	5	1	RELI_LITRU
7	6	40.0	5	1	TRM3_ECOLI
8	6	40.0	5	1	UXA4_CHUTR
9	6	40.0	6	1	ASP2_LACSN
10	6	40.0	6	1	TRPI_PSEPU
11	6	40.0	7	1	ALL4_CARMA
12	6	40.0	7	1	ALL7_CYPDO
13	6	40.0	7	1	CHOK_ALCSP
14	6	40.0	7	1	FAR1_HELTI
15	6	40.0	7	1	FAR2_PROCL
16	6	40.0	7	1	FAR2_CALVO
17	6	40.0	7	1	UF03_MOUSE
18	6	40.0	7	1	UF04_MOUSE
19	6	40.0	8	1	ACT_THRAL
20	6	40.0	8	1	ACT_THRAL
21	6	40.0	8	1	AKH_MELML
22	6	40.0	8	1	AL12_CARMA
23	6	40.0	8	1	AL12_CARMA
24	6	40.0	8	1	ALL4_CALVO
25	6	40.0	8	1	ALL5_CALVO
26	6	40.0	8	1	ALL5_CYPDO
27	6	40.0	8	1	ANG2_BOTJU
28	6	40.0	8	1	CCRN_MACEU
29	6	40.0	8	1	COXG_RAT
30	6	40.0	8	1	FAR1_PANRE
31	6	40.0	8	1	FAR2_HOMAM
32	6	40.0	8	1	FAR2_CALVO
33	6	40.0	8	1	GLUR_HUMAN

34	6	40.0	8	1	LCR1_LEUMA	P21140 leucophaea
35	6	40.0	8	1	LCR2_LEUMA	P21141 leucophaea
36	6	40.0	8	1	LCR3_LEUMA	P21142 leucophaea
37	6	40.0	8	1	LCR4_LEUMA	P21143 leucophaea
38	6	40.0	8	1	LCR7_LEUMA	P19989 leucophaea
39	6	40.0	8	1	LCR8_LEUMA	P19990 leucophaea
40	6	40.0	8	1	LMT2_LOCLI	P22396 locusta mly
41	6	40.0	8	1	ORMY_ORCLI	P82455 orcoptes
42	6	40.0	8	1	PLP_BRANA	P81707 brassica na
43	6	40.0	8	1	UCP6_MAIZE	P80632 zea mays (m
44	6	40.0	8	1	UPA1_HUMAN	P30087 homo sapien
45	6	40.0	9	1	COM_CONVE	P83047 conus ventr

ALIGNMENTS

RESULT 1
LUXE_VIBFI
ID LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl)-protein synthetase (Fragment).
GN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Maignan E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination site for the lux operon."
RL J. Bacteriol. 172:6797-6802(1990).
CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID. IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -1- CATABOLIC ACTIVITY: ATP + an acid + protein -> AMP + diphosphate + an acyl-protein thioester.
CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
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CC EMBL; M62812; -; NOT_ANNOTATED_CDS.
DR Luminescence; Ligase.
KW NON_TER
FT SEQUENCE 3 AA; 374 MM; 6AA3303000000000 CRC64;
SQ
Query Match 40.0%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 D 10
Db 3 D 3
RESULT 2
ACH1_ACHFU
ID ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUN-1998 (Rel. 36, Last annotation update)
 OS Achatin-I.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylomatophora;
 OC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN-Ferussac; TISSUE-Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kametani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Il P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.,
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 fulica ferussac containing a D-amino acid residue."
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN-Ferussac; TISSUE-Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.,
 RT "Purification of achatin-I from the atria of the African giant snail,
 Achatina fulica, and its possible function."
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.,
 RT "Crystal structure and molecular conformation of achatin-I
 (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 D-amino acid residue."
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR: A32460; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C81000000 CRC64;
 D-PHENYLANINE.
 Query Match 40.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 4 D 4
 RESULT 3
 OCP1_OCTMI STANDARD; PRT: 4 AA.
 AC P58648;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 CC Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE-Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.,
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 Octopus minor."
 RL Peptides 21:623-630(2000).
 CC -I- FUNCTION: Cardioactive; has both positive chronotropic and
 inotropic effects on the heart. Ocp-4 is a 1000 time less
 active than Ocp-3.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -I- MASS SPECTROMETRY: MW=395.2; METHOD-WALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B81000000 CRC64;
 D-SERINE (IN OCP-4).
 Query Match 40.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 4 D 4

CC Inotropic effects on the heart. Ocp-2 is a 1000 time less
 active than Ocp-1.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -I- MASS SPECTROMETRY: MW=395.2; METHOD-WALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2
 SQ SEQUENCE 4 AA; 394 MW; 6AA879C81000000 CRC64;
 D-PHENYLANINE.
 Query Match 40.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 4 D 4
 RESULT 4
 OCP3_OCTMI STANDARD; PRT: 4 AA.
 AC P58649;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-3/Ocp-4.
 OS Octopus minor (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 CC Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE-Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.,
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 Octopus minor."
 RL Peptides 21:623-630(2000).
 CC -I- FUNCTION: Cardioactive; has both positive chronotropic and
 inotropic effects on the heart. Ocp-4 is a 1000 time less
 active than Ocp-3.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -I- MASS SPECTROMETRY: MW=395.2; METHOD-WALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B81000000 CRC64;
 D-SERINE (IN OCP-4).
 Query Match 40.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 4 D 4
 RESULT 5
 BIOA_CITFR STANDARD; PRT: 5 AA.
 AC P13071;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
 (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
 aminotransferase) (Fragment).
 GN BIOA.
 OS Citrobacter freundii.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]

RP SEQUENCE FROM N.A.
 RA MEDLINE-8906280; PubMed-2971595;
 RX Shihuan D., Campbell A.;
 RT "Transcriptional regulation and gene arrangement of *Escherichia coli*,
 RT *Citrobacter freundii* and *Salmonella typhimurium* biotin operons.";
 RL Gene 67:203-211(1988).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: Biotin biosynthesis.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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 CC -----
 DR EMBL: M21922; -; NOT_ANNOTATED_CDS.
 DR Interpro: IPR000954; AminoTran_3.
 DR PROSITE: PS00600; AA_TRANSF_CLASS_3; PARTIAL.
 KM Biotin biosynthesis; Transferase; Amino transferase;
 KM Pyridoxal phosphate.
 FT NON_TER
 SQ SEQUENCE 5 AA: 582 MW: 6AABAB1B1A6F00000 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 4 D 4

RESULT 6
 REL_LITRU STANDARD; PRT; 5 AA.
 AC P82070;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodytidae; Litoria.
 OC NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RA Steinboerner S.T., Wadnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog *Litoria rubella*, the skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
 RT Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=598; METHOD-FAB.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA: 598 MW: 6DD9C9CAB2A00000 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 2 D 2

RESULT 7
 TRM3_ECOLI STANDARD; PRT; 5 AA.
 AC P13973;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Trm protein (Fragment).
 OS *Escherichia coli*.
 GN Plasmid IncpII R100.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88227859; PubMed-2836369;
 RA Inamoto S., Yoshioke Y., Ohtsuda E.;
 RT Identification and characterization of the products from the trm and trm genes of Plasmid R100.";
 RL J. Bacteriol. 170:2749-2757(1988).
 CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: TO TRM PROTEIN OF OTHER PLASMIDS.
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 CC -----
 DR EMBL: M20941; -; NOT_ANNOTATED_CDS.
 DR PIR: A32014; A32014.
 KM Conjugation; Plasmid; DNA-binding.
 FT NON_TER
 SQ SEQUENCE 5 AA: 634 MW: 6B1B1AA443500000 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 3 D 3

RESULT 8
 UX4A_CHLTR STANDARD; PRT; 5 AA.
 AC P38005;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OC NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-L2/434/Bu;
 RA Binl E., Santucci A., Magl B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christensen G., Birkelund S., Vetreu E., Ratli G., Pallini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
 DR Stena-2DPAGE: P38005; -.
 FT NON_TER 5
 SQ SEQUENCE 5 AA: 474 MW: 75BAA865AA800000 CRC64;
 Query Match
 Best Local Similarity 40.0%; Score 6; DB 1; Length 5;
 Matches 1; Conservative 100.0%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 4 D 4

RESULT 9
 ASP2_LACSN STANDARD; PRT: 6 AA.
 ID ASP2_LACSN
 AC P82655;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acid shock protein 2 (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 NC NCB1_TaxID=1625;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=CBI;
 RX MEDLINE=21322712; PubMed=11429463;
 RA De Angelis M., Bini L., Pallini V., Coccocelli P.S., Gobetti M.;
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
 RL Microbiology 147:1863-1873(2001).
 CC -1- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
 FT NON_TER 6
 SQ SEQUENCE 6 AA: 778 MW: 6AA45B5B132A8000 CRC64;
 Query Match
 Best Local Similarity 40.0%; Score 6; DB 1; Length 6;
 Matches 1; Conservative 100.0%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 6 D 6

RESULT 10
 TRP1_PSEPU STANDARD; PRT: 6 AA.
 ID TRP1_PSEPU
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TRPBA operon transcriptional activator (Fragment).
 GN TRP1.
 OS Pseudomonas putida.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NC NCB1_TaxID=303;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEGI C15;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas putida.";
 RL Blochimie 71:521-531(1989).
 CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

CC -----
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 CC -----
 DR EMBL: X13299; CAA31660.1; -.
 DR InterPro: IPR000847; HTH_LysR.
 DR PROSITE: PS00044; HTH_LYSR_FAMILY, PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA: 683 MW: 77672AA1EDD6F000 CRC64;
 Query Match
 Best Local Similarity 40.0%; Score 6; DB 1; Length 6;
 Matches 1; Conservative 100.0%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 4 D 4

RESULT 11
 ALI4_CARMA STANDARD; PRT: 7 AA.
 ID ALI4_CARMA
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carinustatin 4.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 NC NCB1_TaxID=6759;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RT Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTROPHIC OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA: 782 MW: 672879CDB476AC0 CRC64;
 Query Match
 Best Local Similarity 40.0%; Score 6; DB 1; Length 7;
 Matches 1; Conservative 100.0%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 DB 1 D 1

RESULT 12
 ALL7_CYPDPO STANDARD; PRT: 7 AA.
 ID ALL7_CYPDPO
 AC P82158;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydlastratin 7.
 OS Cydia pomonella (Coddling moth).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

OC Dityrist: Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN (1)
 RP SEQUENCE.
 RC TISSUE-Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Davey H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RT "Leptodactylus peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;
 Query Match 40.0%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 Db 4 D 4

RESULT 13
 CHOX_ALCSP STANDARD; PRT; 7 AA.
 ID P16101;
 AC 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Choline oxidase (EC 1.1.3.17) (Fragment).
 OS Alcaligenes sp.
 OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 OC Alcaligenes
 NCBI_TaxID=512;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=81006769; PubMed=6997283;
 RA Ohta-Fukuyama M., Miyake Y., Eml S., Yamano T.;
 RT "Identification and properties of the prosthetic group of choline
 oxidase from Alcaligenes sp.";
 RL J. Biochem. 88:197-203(1980).
 CC -1- CATALYTIC ACTIVITY: Choline + O(2) -> betaine aldehyde + H(2)O(2).
 DR PIR: A15398.
 KW Oxidoreductase.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;
 Query Match 40.0%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 Db 1 D 1

RESULT 14
 FARL_HELTI STANDARD; PRT; 7 AA.
 ID P41871;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GDPPLRF-amide.
 OS Helisoma trivolvis (Snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Planorbidae; Helisoma.
 NCBI_TaxID=27815;
 RN (1)
 RP SEQUENCE.
 RC TISSUE-Kidney;

RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC THE KIDNEY, MANTLE AND SKIN.
 CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
 Query Match 40.0%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 Db 2 D 2

RESULT 15
 FAR2_PROCL STANDARD; PRT; 7 AA.
 ID P38498;
 AC 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog DF2.
 OS Procambarus clarkii (Red swamp crayfish).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Astacidea; Astacoidea; Cambaridae; Procambarus.
 NCBI_TaxID=6728;
 RN (1)
 RP SEQUENCE.
 RC TISSUE-Pericardial organs;
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tedrugge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 pericardial organs.";
 RL Peptides 14:137-143(1993).
 CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
 Query Match 40.0%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 D 10
 Db 1 D 1

Search completed: June 5, 2003, 15:56:34
 Job time : 7.5155 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:32:58 ; Search time 29.0909 Seconds

(without alignments)
70.829 Million cell updates/sec

Title: US-09-150-947f-15

Perfect score: 15

Sequence: 1 xxxxxxxxxd 10

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organella:*
10: sp_phage:*
11: sp_plant:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	6	40.0	5 2 P83073	P83073 bacillus ce
2	6	40.0	7 2 007354	007354 synechococ
3	6	40.0	7 5 P83274	P83274 macrobrach
4	6	40.0	7 6 Q28742	Q28742 otycolagus
5	6	40.0	7 10 049223	049223 glycine max
6	6	40.0	7 11 063480	063480 rattus norv
7	6	40.0	7 11 055184	055184 rattus norv
8	6	40.0	2 0921E9	0921E9 neisseria m
9	6	40.0	8 2 085406	085406 coxiella bu
10	6	40.0	8 2 09RQ57	09RQ57 buchnera ap
11	6	40.0	8 2 09RQ49	09RQ49 buchnera ap
12	6	40.0	8 2 09R772	09R772 escherichia
13	6	40.0	8 2 P72279	P72279 rhodococcus
14	6	40.0	8 2 056759	056759 xanthobacte
15	6	40.0	8 2 P83158	P83158 anabaena sp
16	6	40.0	8 2 051594	051594 escherichia

17	6	40.0	8 2 0935R0	0935R0 staphylococ
18	6	40.0	8 2 P83152	P83152 anabaena sp
19	6	40.0	8 2 09R3X0	09R3X0 planktothrix
20	6	40.0	8 2 053790	053790 streptococ
21	6	40.0	8 2 08R5R3	08R5R3 lactobacill
22	6	40.0	8 3 09HDS4	09HDS4 aspergillus
23	6	40.0	8 3 09URB9	09URB9 saccharomyc
24	6	40.0	8 4 09P285	09P285 homo sapien
25	6	40.0	8 4 09U500	09U500 homo sapien
26	6	40.0	8 4 09HAD3	09HAD3 homo sapien
27	6	40.0	8 4 015895	015895 homo sapien
28	6	40.0	8 4 015900	015900 homo sapien
29	6	40.0	8 4 015902	015902 homo sapien
30	6	40.0	8 4 09UMC7	09UMC7 homo sapien
31	6	40.0	8 4 09UMH9	09UMH9 homo sapien
32	6	40.0	8 4 09UD24	09UD24 homo sapien
33	6	40.0	8 4 09PDK3	09PDK3 homo sapien
34	6	40.0	8 4 09BYR5	09BYR5 homo sapien
35	6	40.0	8 5 09NGM5	09NGM5 toxoplasma
36	6	40.0	8 5 09UB13	09UB13 albinaria h
37	6	40.0	8 5 094695	094695 physarum po
38	6	40.0	8 5 P83195	P83195 perkinsus a
39	6	40.0	8 5 P83275	P83275 macrobrachl
40	6	40.0	8 5 P83316	P83316 penaeus mon
41	6	40.0	8 5 09TWH6	09TWH6 perinereis
42	6	40.0	8 5 P82686	P82686 periplaneta
43	6	40.0	8 5 P82687	P82687 periplaneta
44	6	40.0	8 6 09T778	09T778 canis fami
45	6	40.0	8 6 08WMS1	08WMS1 bos taurus

ALIGNMENTS

RESULT 1

P83073 ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TREMUREL. 18, Created)
DT 01-OCT-2001 (TREMUREL. 18, Last sequence update)
DT 01-OCT-2001 (TREMUREL. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID:1396.
RN [1]
RP
RC STRAIN-NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AA336F00000 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 3 D 3

RESULT 2

007354 ID 007354 PRELIMINARY; PRT; 7 AA.
AC 007354;
DT 01-JUL-1997 (TREMUREL. 04, Created)
DT 01-JUL-1997 (TREMUREL. 04, Last sequence update)
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE N1fk (Fragment).
GN N1fk.
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanophyceae PCC 8801).

OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 OX NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RF-1;
 RX MEDLINE=99231861; PubMed=10217509;
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic
 RT nitrogen-fixing unicellular cyanobacterium *Synechococcus* sp. strain
 RT RF-1.";
 RL Microbiology 145:743-753(1999).
 DR EMBL; AF003700; AAC35193.1; -.
 FT NON-TER 1
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
 Query Match 40.0%; Score 6; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 P83274 PRELIMINARY; PRT; 7 AA.
 AC P83274;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE FMRamide-like neuropeptide F1P1 (DRNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonidae; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=EYESTALK;
 RA Sitthigorngul P., Sarathongkum W., Jaldechoey S., Longyant S.,
 RA Sitthigorngul W.;
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn *Macrobrachium rosenbergii*.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -1- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CM Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
 Query Match 40.0%; Score 6; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 Q28742 PRELIMINARY; PRT; 7 AA.
 ID Q28742;
 AC Q28742;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL; K01698; AAA31415.1; -.
 FT NON-TER 1
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
 Query Match 40.0%; Score 6; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 O49223 PRELIMINARY; PRT; 7 AA.
 AC O49223;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HMG-1-like protein (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ESSEX; TISSUE=ROOT;
 RX MEDLINE=91367679; PubMed=1891369;
 RA Laux T., Goldberg R.B.;
 RT "A plant DNA binding protein shares highly conserved sequence motifs
 RT with HMG-box proteins.";
 RL Nucleic Acids Res. 19:4769-4769(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ESSEX; TISSUE=ROOT;
 RA Mahalingam R., Knapp H.T.;
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF047050; AAC03556.1; -.
 FT NON-TER 1
 SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;
 Query Match 40.0%; Score 6; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 Q63480 PRELIMINARY; PRT; 7 AA.
 ID Q63480;
 AC Q63480;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE TR4-NS orphan receptor (Fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96198747; PubMed-8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RT Detera-Wadleigh S.D.:
 "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain."
 RT domain."
 RL Endocrinology 137:1562-1571(1996).
 DR EMBL: U59125; AAB02827.1; -
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 7 AA; 758 MW; 672AAB7864005350 CRC64;

Query Match 40.0%; Score 6; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 6 D 6

RESULT 7
 ID 055184 PRELIMINARY; PRT; 7 AA.
 AC 055184;
 DT 01-JUN-1998 (TRENBLREL. 06, Created)
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Orphan receptor TR4-NS (Fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-96198747; PubMed-8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RT Detera-Wadleigh S.D.:
 "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain."
 RT domain."
 RL Endocrinology 137:1562-1571(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-96299786; PubMed-8661150;
 RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.:
 "New variants of the human and rat nuclear hormone receptor, TR4:
 expression and chromosomal localization of the human gene."
 RT Genomics 35:361-366(1996).
 DR EMBL: U59454; AAB91433.1; -
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 40.0%; Score 6; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 6 D 6

RESULT 8
 ID 0921E9 PRELIMINARY; PRT; 8 AA.
 AC 0921E9;
 DT 01-MAY-1999 (TRENBLREL. 10, Created)

DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
 DT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)
 DE Carbamoyl-phosphate synthase subunit B (Fragment).
 GN CARB
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID-487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1527;
 RX MEDLINE-95291461; PubMed-7773412;
 RA Lawson F.S., Billowes F.M., Dillon J.A.:
 "Organization of carbamoyl-phosphate synthase genes in Neisseria
 gonorrhoeae includes a large, variable intergenic sequence which is
 also present in other Neisseria species."
 RT Microbiology 141:0-0(0).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1527;
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.:
 "Complexity of the variable sequence between the carbamoyl-phosphate
 synthase genes of Neisseria species."
 RT Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF029361; AAC78449.1; -
 KW NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 6 D 6

RESULT 9
 ID 085406 PRELIMINARY; PRT; 8 AA.
 AC 085406;
 DT 01-NOV-1998 (TRENBLREL. 08, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 OS Coxiella burnetii.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 OC Coxiella group; Coxiella.
 OC NCBI_TaxID-777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NINE MILE PHASE I;
 RX MEDLINE-98348442; PubMed-9683477;
 RA Williams H., Jaeger C., Baljer G.:
 "Physical and genetic map of the obligate intracellular bacterium
 Coxiella burnetii."
 RT J. Bacteriol. 180:3816-3822(1998).
 RL EMBL: AF064963; AAD09947.1; -
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 DB 6 D 6

RESULT 10
 ID 09R057 PRELIMINARY; PRT; 8 AA.
 AC 09R057

AC 09R057;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN NIFS.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 RT compositions.";
 RL Mol. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AF130812; AAF13797.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 8 D 8

RESULT 11

09R049 PRELIMINARY; PRT; 8 AA.
 ID 09R049;
 AC 09R049;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN NIFS.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 RT compositions.";
 RL Mol. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AF130814; AAF13805.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 8 D 8

RESULT 12

09R772 PRELIMINARY; PRT; 8 AA.
 ID 09R772;
 AC 09R772;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 GN YQFG.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aida H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horuchi T.;
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
 RT to the 12,7-28.0 mln Region on the Linkage Map.";
 RL DNA Res. 3:137-155(1996).
 DR EMBL; D90705; BAA5310.1; -.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 1 D 1

RESULT 13

P72279 PRELIMINARY; PRT; 8 AA.
 ID P72279;
 AC P72279;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Biphenyl dioxygenase (Fragment).
 GN BPHB.
 OS Rhodococcus globerulus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Rhodococcus.
 OX NCBI_TaxID=33008;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95255652; PubMed=7737502;
 RA Asturias J.A., Diaz E., Timmis K.N.;
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
 RT positive bacterium Rhodococcus globerulus p6 to multicomponent
 RT dioxygenases of gram-negative bacteria.";
 RL Gene 156:11-18(1995).
 DR EMBL; X80041; CAA56350.1; -.
 KW Dioxygenase.
 FT NON_TER
 SQ SEQUENCE 8 AA; 989 MW; EBD2C81AB6D73406 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
 DB 5 D 5

RESULT 14

056759 PRELIMINARY; PRT; 8 AA.
 ID 056759;
 AC 056759;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Halocacid dehalogenase (Fragment).
 GN DHB.
 OS Xanthobacter autotrophicus.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Hypnomicrobium group; Xanthobacter.
 OX NCBI_TaxID=280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GJ10, AND CV. M50;
 RX MEDLINE-95173113; PubMed-7868610;
 RA Van der Ploeg J., Willemse M., van Hall G., Janssen D.B.;
 RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
 RT activation and mobilization of the haloacetate dehalogenase gene by
 RT insertion element IS1247";
 RL J. Bacteriol. 177:1348-1356(1995).
 DR EMBL; X84038; CAA5857.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD3056 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 8 D 8

RESULT 15

P83158 PRELIMINARY; PRT; 8 AA.
 ID P83158;
 AC P83158;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
 DE Photosystem I Iron-sulfur center (Photosystem I subunit VII) (9 kDa
 DE polypeptide) (PSI-C) (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apte S.K., Uhlemann E., Schmid R., Alendroff K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.
 CC -I- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE
 CC PHOTOSYSTEM I COMPLEX.
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -I- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
 CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
 DR InterPro: IPR001450; 4Fe4S_Ferredoxin.
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; PARTIAL.
 KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.
 FT NON_TER
 SQ SEQUENCE 8 AA; 962 MW; C5B50532D1A1F5 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
 |
 Db 8 D 8

Search completed: June 5, 2003, 15:55:44
 Job time : 30.0909 secs

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XX Claim 2; Fig 2; 72pp; English.
 PS
 CC The present sequence represents the SMEZ-2 superantigen protein. The
 CC specification describes superantigen proteins SMEZ-2, SPE-G, SPE-H
 CC and SPE-J. The superantigen polynucleotides and polypeptides are
 CC used for subtyping Streptococci. They are also used for diagnosing
 CC Streptococcal disease. The superantigens are used in diagnosis of
 CC disease such as Kawasaki syndrome. They are also useful to recruit
 CC and activate T cells in a relatively non-specific fashion since
 CC they bind a large number of T cell receptor molecules by binding to the
 CC Vbeta domain. Superantigen constructs are useful in cancer therapy.
 SQ Sequence 233 AA;
 QY Query Match 72.7%; Score 24; DB 21; Length 233;
 Best Local Similarity 50.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 DB 3 KXXXTXQEXD 12
 149 KTTVTAQED 158
 RESULT 2
 ABP29565
 ID ABP29565 standard; Protein; 258 AA.
 AC ABP29565;
 XX
 DT 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 8306.
 XX
 KM Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; Infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Maignant V, Margalit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN70196.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 1; Page 3947; 4525pp; English.
 PS
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5463 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 SQ Sequence 258 AA;
 QY Query Match 72.7%; Score 24; DB 23; Length 258;
 Best Local Similarity 50.0%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 DB 3 KXXXTXQEXD 12
 174 KTTVTAQED 183
 RESULT 3
 ABB76254
 ID ABB76254 standard; Peptide; 17 AA.
 AC ABB76254;
 XX
 DT 09-AUG-2002 (first entry)
 DE Staphylococcus aureus enterotoxin C1 peptide fragment.
 XX
 KM Enterotoxin C; SECI; superantigen; antigen; tumour; cancer;
 KM antitumour; therapy.
 XX
 OS Staphylococcus aureus.
 XX
 PM US2002051765-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 19-DEC-2000; 2000US-0741503.
 XX
 PR 31-JAN-1994; 94US-0189424.
 PR 19-JUN-1995; 95US-0491746.
 PR 03-OCT-1989; 89US-0416530.
 PR 17-JAN-1990; 90US-0466577.
 PR 17-JAN-1991; 91WO-US00342.
 PR 01-JUN-1992; 92US-0891718.
 PR 02-MAR-1993; 93US-0025144.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI: 2002-415198/44.
 XX
 PT Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens -
 XX
 PS Disclosure; Page 4; 17pp; English.
 PS
 CC The present sequence corresponds to amino acids 151-167 of
 CC enterotoxin C1 (SECI, see ABB76238) of Staphylococcus aureus.
 CC Sequence similarities are found in the corresponding regions
 CC of other staphylococcal enterotoxins and streptococcal pyrogenic
 CC exotoxins (see ABB76252-59). In the present invention, synthetic
 CC polypeptides useful in tumour therapy and in blocking or destroying
 CC autoreactive T and B lymphocyte populations are characterised by
 CC substantial structural homology to staphylococcal enterotoxin A and
 CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with
 CC statistically significant sequence homology and similarity,
 CC including alignment of cysteine residues and similar hydropathy


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CC profiles. These superantigens are used to treat solid tumours,  
CC including their metastases, without radiation, surgery or standard  
CC chemotherapeutic agents. A claimed method of human cancer treatment  
CC involves contacting haematopoietic cells from a patient with one or  
CC more superantigens ex vivo to generate stimulated cells, selecting  
CC a specific V beta subset of cells, and reintroducing these cells  
CC into the patient to induce an in vivo therapeutic, tumouricidal  
CC reaction.  
XX  
XX .Sequence      17 AA:  
SQ  
  
Query Match          69.7%; Score 23; DB 23; Length 17;  
Best Local Similarity 50.0%; Pred. No. 9.8;  
Matches      5; Conservative    0; Mismatches     5; Indels     0; Gaps     0  
              3 KKKXTXQEXD 12  
                |   |   |  
Db             1 KKSVAQELD 10  
  
RESULT 4  
AAAY97855  
AC  AAAY97855; peptide: 24 AA.  
XX  
XX 29-AUG-2000 (first entry)  
XX  
DE Staphylococcus aureus enterotoxin SEC, conserved region 2.  
XX  
KW Staphylococcal infection; enterotoxin; septic shock; toxic shock;  
KM vaccine; antibody.  
OS Staphylococcus aureus.  
PN W0200020598-A1.  
PD 13-APR-2000.  
PF 24-SEP-1999; 99WO-US22180.  
PR 07-OCT-1998; 98US-0168303.  
PR 18-JUN-1999; 99US-0335581.  
PA (UYRQ ) UNIV ROCKEFELLER.  
PI Bannan JD, Visvanathan K, Zabriskie JB;  
DR WPI: 2000-303782/26.  
XX  
XX Peptides useful for preventing and reducing the symptoms of toxic shock  
PT syndrome and septic shock from staphylococcal and streptococcal  
PT infections -  
XX  
XX Example 1: Page 72; 115pp; English.  
XX  
XX The invention relates to novel peptides (AAAY97838-Y97843) comprising a  
CC consensus amino acid sequence derived from two conserved regions  
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and  
CC streptococcal pyrogenic toxin. Consensus region 1a (a preferred  
CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N  
CC (AAAY97863) and consensus region 2a (a preferred consensus region 2) has  
CC the sequence K-X6-X7-X8-  
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y  
CC (AAAY97864), where: X1, X8, X13 and X24 are each independently selected  
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,  
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from  
CC the group consisting of any amino acid;  
CC X3, X5 and X26 are each independently selected from the group consisting  
CC of any amino acid and of no amino acid;  
CC X27 is either L or Y.  
XX The invention also relates to serum antibodies induced by the peptides  
CC which provide protection against, or reduce the severity of toxic shock
```

CC	pyrogenic shock caused by the staphylococcal and streptococcal
CC	pyrogenic toxins. The pyrogenic exotoxins of group A streptococci and
CC	the enterotoxins of Staphylococcus aureus (which are also pyrogenic
CC	exotoxins) constitute a family of structurally related toxins which
CC	share similar biological activities. They stimulate CD4+, CD8+ and
CC	gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
CC	elements on the lateral face of the T-cell receptor (TCR) while
CC	simultaneously binding the lateral face of the class II major
CC	histocompatibility complex (MHC) of antigen presenting cells. This causes
CC	aberrant proliferation of T-cells, which stimulates other components of
CC	the immune system, causing injury to the host. The peptides are used to
CC	prevent, treat or protect against toxic shock and septic shock resulting
CC	from bacterial infections in mammals, particularly humans. The peptides
CC	are used for inducing serum antibodies that bind at least one
CC	staphylococcal enterotoxin or streptococcal exotoxin and both the
CC	peptides and antibodies can be used in diagnostic assays to aid in the
CC	diagnosis of disease related to the presence of bacterial toxins. Nucleic
CC	acids encoding a peptide of the invention can be used for the production
CC	of the peptides for diagnostic reagents, as vaccines and for therapies
CC	for pyrogenic exotoxin related diseases. Vectors expressing high levels
CC	of the peptides can be used in immunotherapy and immunoprophylaxis when
CC	expressed in humans. The antibodies are used for passive immunisation
CC	therapy to prevent or increase resistance to toxic shock syndrome or
CC	septic shock and to ameliorate the effects of conditions associated with
CC	the presence of staphylococcal or streptococcal pyrogenic toxins. The
CC	amino acid sequences of the peptides are sufficiently common that they
CC	can be used for eliciting antibodies which are cross-reactive with toxins
CC	derived from various bacteria. Sequences AAY97853-Y97861 represent
CC	conserved region 2 of various Staphylococcus aureus enterotoxins and
CC	group A streptococcal pyrogenic exotoxins.
CC	xx
SO	Sequence 24 AA:
SO	Query Match 69.7%; Score 23; DB 21; Length 24;
SO	Best Local Similarity 50.0%; Pred. No. 14;
SO	Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0.
OY	3 KXXXTXQEXD 12
	1 1 1 1
Db	1 KKSVTQAEILD 10
RESULT 5	
AAY72193	
ID	AAY72193 standard; peptide; 24 AA.
xx	
xx	AAY72193;
xx	
DT	24-APR-2001 (first entry)
xx	
DE	Peptide from region 2 of staphylococcal enterotoxin SEC.
xx	
KW	Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
KW	staphylococcal enterotoxin; human immunodeficiency virus; T cell;
KW	autoimmune disease; immunisation.
xx	
xx	Staphylococcus sp.
xx	
OS	
PN	WO200078790-A2.
xx	
PD	28-DEC-2000.
xx	
PF	16-JUN-2000; 2000WO-US16680.
xx	
PR	18-JUN-1999; 99US-0336627.
xx	
XX	(UYRQ) UNIV ROCKEFELLER.
xx	
PA	Visvanathan K, Zabriskie JB;
xx	
PI	WPI: 2001-080820/09.
xx	
DR	
xx	
PT	Providing protection against, and reducing the severity of, human

immunodeficiency virus infections and associated deleterious effects, using peptides from homologous sequences of staphylococcal and streptococcal toxins

Disclousure; Page 36; 76pp; English.

The present sequence is a peptide from region 2 of staphylococcal enterotoxin SEC.

The peptide, nucleic acid encoding the peptide and antibody (Ab) produced against the peptide are useful for inhibiting blastogenesis of mononuclear cells (eg. T cells) in the presence of human immunodeficiency virus (HIV), inhibiting HIV replication and protecting a mammal against the deleterious effects of HIV. The peptide is also used to ameliorate the effects of autoimmune diseases associated with the presence of HIV. The Ab is used for passively immunising a mammal against the deleterious effects of HIV.

Sequence 24 AA;

Query Match 69.7%; Score 23; DB 22; Length 24;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 1 KKSVAQDEL 10

RESULT 6
AAM59147
ID AAM59147 standard; Protein; 29 AA.

AAM59147;
05-NOV-2001 (first entry)

Human brain expressed single exon probe encoded protein SEQ ID NO: 31252.

Human; brain expressed; exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

Homo sapiens.

MO200157275-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00667.

04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-483446/52.

Single exon nucleic acid probes for analyzing gene expression in human brains -

Example 4; SEQ ID NO: 31252; 650pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system

diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.

Sequence 29 AA;

Query Match 69.7%; Score 23; DB 22; Length 29;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 10 KALSTGQELD 19

RESULT 7
AAM71683
ID AAM71683 standard; Protein; 29 AA.

AAM71683;
06-NOV-2001 (first entry)

Human bone marrow expressed probe encoded protein SEQ ID NO: 31989.

Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukemia; lymphoma; myeloma.

Homo sapiens.

WO200157276-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00668.

04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -

Example 4; SEQ ID NO: 31989; 658pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.

Sequence 29 AA;

Query Match 69.7%; Score 23; DB 22; Length 29;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 10 KALSTGQELD 19

RESULT 8
 AAM31976
 ID AAM31976 standard; Protein: 29 AA.
 XX
 AC AAM31976;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #6013 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -
 XX
 PS Claim 27; SEQ ID NO 32245; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see A131315-A157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SQ Sequence 29 AA:
 Query Match 69.7%; Score 23; DB 22; Length 29;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 3 KAXXTXQEXD 12
 DB 10 KALSTGOEID 19
 RESULT 9
 ABG41496
 ID ABG41496 standard; Peptide: 29 AA.
 XX
 AC ABG41496;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 31161.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00665.
 XX
 PR 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples -
 XX
 PS Claim 27; SEQ ID NO 31161; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression to a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 29 AA;
 Query Match 69.7%; Score 23; DB 23; Length 29;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXXXTXQEXD 12
 DB 10 KALSTGQELD 19
 RESULT 10
 AAG63856
 ID AAG63856 standard; Protein: 228 AA.
 AC AAG63856;
 DT 29-OCT-2001 (first entry)
 DE Amino acid sequence of a modified Staphylococcal enterotoxin C1.
 XX
 XX Enterotoxin C1; SEC-SER; Infectious disease; mastitis.
 OS Synthetic.
 OS Staphylococcus sp.
 XX WO200160851-A1.
 PN 23-AUG-2001.
 PD 31-OCT-2000; 2000WO-KR01241.
 PF 17-FEB-2000; 2000KR-0007612.
 PR (GLDS) LG CHEM LTD.
 XX
 PA Lee H, Park Y, Han K, Chang B, Lee Y;
 PI WPI: 2001-522585/57.
 DR N-PSDB: AAH74983.
 XX
 DR Producing stable modified Staphylococcal toxin polypeptide for treating
 PT infectious diseases, e.g. mastitis, in animals, involves substituting
 PT cysteine at specified position of modified Staphylococcal toxin C1 with
 PT serine -
 PS Claim 1; Page 59-60; 64pp; English.
 XX
 XX The present sequence represents a modified Staphylococcal enterotoxin C1,
 CC designated SEC-SER. The modified toxin is characterised in that the
 CC 95th amino acid (cysteine) is substituted with serine. This results in
 CC a toxin that has improved stability. The modified enterotoxin is
 CC useful for preventing or treating infectious diseases due to
 CC microorganisms in animals such as cows, pigs, horses, sheep, hens,
 CC dogs and cats, e.g. mastitis in cows.
 XX
 SQ Sequence 228 AA;
 Query Match 69.7%; Score 23; DB 22; Length 228;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXXXTXQEXD 12
 DB 140 KKSVTAGQELD 149
 RESULT 11
 AAR13208
 ID AAR13208 standard; Protein: 238 AA.
 AC AAR13208;
 XX

DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin C3.
 XX
 XX SEC3; cancer treatment; pyrogen; tumouricide.
 KW
 XX Staphylococcus aureus.
 OS
 XX WO9110680-A.
 PN 25-JUL-1991.
 PD 17-JAN-1991; 91WO-US00342.
 PF 17-JAN-1990; 90US-046577.
 PR (TERM/) TERMAN D S.
 PA Terman DS;
 PI WPI: 1991-237984/32.
 DR
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 XX
 XX Disclosure: Fig 1; 74pp; English.
 PS
 XX SEC3 was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophaty profiles.
 CC See AAR13203-R13211.
 XX
 SQ Sequence 238 AA;
 Query Match 69.7%; Score 23; DB 12; Length 238;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXXXTXQEXD 12
 DB 150 KKSVTAGQELD 159
 RESULT 12
 AAR45016
 ID AAR45016 standard; Protein: 238 AA.
 AC AAR45016;
 XX
 XX 08-JUN-1994 (first entry)
 DT
 DE Staphylococcal enterotoxin SEC3.
 DE
 XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 KW
 XX Staphylococcus aureus.
 OS
 XX WO9324136-A.
 PN 09-DEC-1993.
 PD 01-JUN-1993; 93WO-US05213.
 PF 01-JUN-1992; 92US-0891718.
 PR
 XX

PA (STON/) STONE J L.
 (TERM/) TERMAN D S.
 XX Stone JL, Terman DS;
 PI WPI: 1993-405418/50.
 DR WPI: 1993-405418/50.
 XX
 XX Use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 XX
 XX Disclosure: Fig 1: 90pp: English.
 PS
 XX The sequences given in AAR45011-21 are staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumoricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumoricidal activity and toxicity identical to that
 CC observed for the Protein A pertussis system. They may be administered
 CC by i.v. injection.
 CC
 SQ Sequence 238 AA:

Query Match 69.7%; Score 23; DB 14; Length 238;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 DB 150 KKSVTQAEID 159

RESULT 13
 AAB67343

ID AAB67343 standard; peptide; 238 AA.

AC AAB67343;

DT 23-APR-2001 (first entry)

DE Staphylococcus aureus enterotoxin C3 protein.

KW Tumour; cancer; immune; enterotoxin.

OS Staphylococcus aureus.

PN US6180097-B1.

PD 30-JAN-2001.

PF 30-OCT-1998; 98US-0183437.

PR 31-JAN-1994; 94US-0189424.

PR 19-JUN-1995; 95US-0491746.

PR 03-OCT-1989; 89US-0416530.

PR 17-JAN-1990; 90US-0466577.

PR 17-JAN-1991; 91WO-0500342.

PR 01-JUN-1992; 92US-0891718.

PR 02-MAR-1993; 93US-0025144.

XX (TERM/) TERMAN D S.

PA Terman DS;

PI WPI: 2001-158657/16.

DR Tumor cell capable of stimulating antitumor immune reactivity in vitro
 XX or in vivo comprises exogenous nucleic acids encoding a superantigen
 XX and a costimulatory molecule -
 XX Disclosure: Fig 2: 16pp: English.
 PS The present invention relates to a tumour cell capable of stimulating
 CC

CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule
 CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 CC
 SQ Sequence 238 AA:

Query Match 69.7%; Score 23; DB 22; Length 238;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 DB 150 KKSVTQAEID 159

RESULT 14
 ABB76239

ID ABB76239 standard; Protein; 238 AA.

AC ABB76239;

DT 09-AUG-2002 (first entry)

DE Staphylococcus aureus enterotoxin C3.

KW Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer;
 antitumour; therapy.

OS Staphylococcus aureus.

FT key location/Qualifiers

FT Misc-difference 208 /note- "given as 'O' in the specification"

PN US2002051765-A1.

PD 02-MAY-2002.

PF 19-DEC-2000; 2000US-0741503.

PR 31-JAN-1994; 94US-0189424.

PR 19-JUN-1995; 95US-0491746.

PR 03-OCT-1989; 89US-0416530.

PR 17-JAN-1990; 90US-0466577.

PR 17-JAN-1991; 91WO-0500342.

PR 01-JUN-1992; 92US-0891718.

PR 02-MAR-1993; 93US-0025144.

XX (TERM/) TERMAN D S.

PA Terman DS;

PI WPI: 2002-415198/44.

DR Reagent for treating cancer without the need for e.g. radiotherapy,
 XX comprises a specific V beta subset of T cells sensitized to a growing
 XX tumor and stimulated with superantigens -
 XX Disclosure: Fig 2: 17pp: English.
 PS The present sequence is the protein sequence of enterotoxin C3
 CC (SEC3) of Staphylococcus aureus. Similarly is shown, in several
 CC stretches of sequence, between staphylococcal enterotoxins,
 CC streptococcal, pyrogenic exotoxins and staphylococcal exfoliative
 CC toxins (see ABB76234-44). In the present invention, synthetic
 CC polypeptides useful in tumour therapy and in blocking or destroying
 CC autoreactive T and B lymphocyte populations are characterised by
 CC substantial structural homology to staphylococcal enterotoxin A and
 CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with

CC statistically significant sequence homology and similarity (Z value
CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding
CC 6) to include alignment of cysteine residues and similar hydrophathy
CC profiles. These superantigens are used to treat solid tumours,
CC including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient
CC with one or more superantigens ex vivo to generate stimulated cells,
CC selecting a specific V beta subset of cells, and reintroducing
CC these cells into the patient to induce an in vivo therapeutic,
CC tumoricidal reaction.

XX
SQ Sequence 238 AA;

Query Match 69.7%; Score 23; DB 23; Length 238;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
| | | |
Db 150 KKSVTQAQELD 159

RESULT 15

AAR13207 standard; Protein; 239 AA.

XX AAR13207;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin C1.

XX SECI; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.

PN W09110680-A.

PD 25-JUL-1991.

PF 17-JAN-1991; 91WO-US00342.

PR 17-JAN-1990; 90US-0466577.

XX (TERM/) TERMAN D S.

PI Terman DS;

DR WPI; 1991-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions

PS Disclosure; Fig 1; 74pp; English.

XX SECI was isolated and purified from S. aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC lipothen to attenuate toxic reaction to SECI. Synthetic
CC polypeptides having structural homology to SECI. Synthetic
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of Cysteine residues and
CC similar hydrophathy profiles.
CC See AAR13203-R13211.

XX
SQ Sequence 239 AA;

Query Match 69.7%; Score 23; DB 12; Length 239;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
| | | |
Db 151 KKSVTQAQELD 160

Search completed: June 5, 2003, 16:00:25
Job time : 40.7273 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:23:33 ; Search time 10.5455 seconds
(without alignments)
33,481 Million cell updates/sec

Title: US-09-150-947F-16
Perfect score: 33
Sequence: 1 XXXXXXTXQEXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	69.7	17	4	US-08-896-933-6
2	23	69.7	17	4	US-09-314-235-6
3	23	69.7	24	3	US-08-838-413A-20
4	23	69.7	238	4	US-08-896-933-28
5	23	69.7	238	4	US-09-314-235-28
6	23	69.7	239	4	US-08-896-933-27
7	23	69.7	239	4	US-09-314-235-27
8	23	69.7	266	4	US-09-144-776B-14
9	22	66.7	17	4	US-08-896-933-4
10	22	66.7	17	4	US-08-896-933-12
11	22	66.7	17	4	US-08-896-933-14
12	22	66.7	17	4	US-08-896-933-15
13	22	66.7	17	4	US-08-896-933-16
14	22	66.7	17	4	US-08-896-933-17
15	22	66.7	17	4	US-09-314-235-4
16	22	66.7	17	4	US-09-314-235-12
17	22	66.7	17	4	US-09-314-235-14
18	22	66.7	17	4	US-09-314-235-15
19	22	66.7	17	4	US-09-314-235-16
20	22	66.7	17	4	US-09-314-235-17
21	22	66.7	24	3	US-08-838-413A-19
22	22	66.7	24	3	US-08-838-413A-24
23	22	66.7	191	4	US-08-858-207A-381
24	22	66.7	221	4	US-08-896-933-29
25	22	66.7	221	4	US-09-314-235-29
26	22	66.7	239	4	US-08-896-933-26
27	22	66.7	239	4	US-09-314-235-26

28	22	66.7	239	4	US-09-144-776B-10	Sequence 10, Appl
29	22	66.7	251	4	US-09-144-776B-16	Sequence 16, Appl
30	22	66.7	255	1	US-08-446-918A-2	Sequence 2, Appl
31	22	66.7	255	2	US-08-580-806-2	Sequence 2, Appl
32	22	66.7	266	4	US-09-414-276-8	Sequence 8, Appl
33	22	66.7	266	4	US-09-144-776B-6	Sequence 6, Appl
34	22	66.7	266	4	US-09-144-776B-8	Sequence 8, Appl
35	22	66.7	292	4	US-09-190-824-2	Sequence 2, Appl
36	22	66.7	922	2	US-08-464-402-2	Sequence 2, Appl
37	22	66.7	922	4	US-09-054-775C-2	Sequence 2, Appl
38	21	63.6	17	4	US-08-896-933-2	Sequence 2, Appl
39	21	63.6	17	4	US-08-896-933-8	Sequence 8, Appl
40	21	63.6	17	4	US-08-896-933-10	Sequence 10, Appl
41	21	63.6	17	4	US-09-314-235-2	Sequence 2, Appl
42	21	63.6	17	4	US-09-314-235-8	Sequence 8, Appl
43	21	63.6	17	4	US-09-314-235-10	Sequence 10, Appl
44	21	63.6	24	3	US-08-838-413A-4	Sequence 4, Appl
45	21	63.6	24	3	US-08-838-413A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-896-933-6
; Sequence 6, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-6
Query Match 69.7%; Score 23; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.86;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 KXXXTXQEXD 12
DB 1 KKSVAQELD 10
RESULT 2
US-09-314-235-6
; Sequence 6, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577

EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 17
TYPE: PRT
ORGANISM: Staphylococcus aureas
US-09-314-235-6

Query Match
Best Local Similarity 69.7%; Score 23; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 0.86;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
DB 1 KKSVTQAEID 10

RESULT 3
US-08-838-413A-20
Sequence 20, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-20

Query Match
Best Local Similarity 69.7%; Score 23; DB 3; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
DB 1 KKSVTQAEID 10

RESULT 4
US-08-896-933-28
Sequence 28, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 238
TYPE: PRT
ORGANISM: Staphylococcus aureas
US-08-896-933-28

Query Match
Best Local Similarity 69.7%; Score 23; DB 4; Length 238;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
DB 150 KKSVTQAEID 159

RESULT 5
US-09-314-235-28
Sequence 28, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 238
TYPE: PRT
ORGANISM: Staphylococcus aureas
US-09-314-235-28

Query Match
Best Local Similarity 69.7%; Score 23; DB 4; Length 238;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
DB 150 KKSVTQAEID 159

RESULT 6

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 27
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

Query Match 69.7%; Score 23; DB 4; Length 239;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEND 12
| | | |
Db 151 KKSXTAQELD 160

RESULT 7
US-09-314-235-27
; Sequence 27, Application US/09314235.
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 27
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-314-235-27

Query Match 69.7%; Score 23; DB 4; Length 239;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEND 12
| | | |
Db 151 KKSXTAQELD 160

RESULT 8
US-09-144-776B-14
; Sequence 14, Application US/09144776B
; Patent No. 6399332

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC-504 Scott Street
MCAR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match 69.7%; Score 23; DB 4; Length 266;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEND 12
| | | |
Db 178 KKSXTAQELD 187

RESULT 9
US-08-896-933-4
; Sequence 4, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 17
; TYPE: PRF
; ORGANISM: Staphylococcus aureus

US-08-896-933-4

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 1 KKNVTAQELD 10

RESULT 10

US-08-896-933-12
Sequence 12, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 17
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-08-896-933-12

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 1 KKNVTAQELD 10

RESULT 11

US-08-896-933-14
Sequence 14, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 17
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
; OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-14

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 1 KKNVTAQELD 10

RESULT 12
US-08-896-933-15
Sequence 15, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 17
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
; OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-15

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 1 KKNVTAQELD 10

RESULT 13

US-08-896-933-16
Sequence 16, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 17
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
; OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-16

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 1 KKNVTAQELD 10

RESULT 14

US-08-896-933-17
Sequence 17, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
;; FILE REFERENCE: 09629/005002
;; CURRENT APPLICATION NUMBER: US/08/896,933
;; CURRENT FILING DATE: 1997-07-18
;; EARLIER APPLICATION NUMBER: 08/252,978
;; EARLIER FILING DATE: 1994-06-02
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 17
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Other
;; FEATURE:
;; OTHER INFORMATION: Consensus sequences derived from staphylococcus
;; OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides
US-08-896-933-17

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTQEXD 12
| | | |
Db 1 KKNVTAQELD 10

RESULT 15
US-09-314-235-4
;; Sequence 4, Application US/09314235
;; Patent No. 6338845
;; GENERAL INFORMATION:
;; APPLICANT: Terman, David S.
;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
;; FILE REFERENCE: 09629/005004
;; CURRENT APPLICATION NUMBER: US/09/314,235
;; CURRENT FILING DATE: 1999-05-18
;; EARLIER APPLICATION NUMBER: 08/896,933
;; EARLIER FILING DATE: 1997-07-18
;; EARLIER APPLICATION NUMBER: 08/252,978
;; EARLIER FILING DATE: 1994-06-02
;; EARLIER APPLICATION NUMBER: 07/891,718
;; EARLIER FILING DATE: 1992-06-01
;; EARLIER APPLICATION NUMBER: US91/00342
;; EARLIER FILING DATE: 1991-01-17
;; EARLIER APPLICATION NUMBER: 07/466,577
;; EARLIER FILING DATE: 1990-01-17
;; EARLIER APPLICATION NUMBER: 07/416,530
;; EARLIER FILING DATE: 1989-10-03
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureas
US-09-314-235-4

Query Match 66.7%; Score 22; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTQEXD 12
| | | |
Db 1 KKNVTAQELD 10

Search completed: June 5, 2003, 15:32:44
Job time : 11.5455 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:01 ; Search time 14.5455 Seconds
(without alignments)
85.173 Million cell updates/sec

Title: US-09-150-947f-16
Sequence: 1 XXXXXXXXQEXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 segs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB pep.*
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7: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB pep.*
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12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	69.7	29	10 US-09-864-761-43487	Sequence 43487, A
2	23	69.7	266	1 US-08-882-431-14	Sequence 14, Appl
3	23	69.7	266	9 US-09-870-759-12	Sequence 12, Appl
4	23	69.7	266	9 US-10-002-784A-14	Sequence 14, Appl
5	22	66.7	10	10 US-09-150-947B-3	Sequence 3, Appl1
6	22	66.7	10	10 US-09-150-947B-4	Sequence 4, Appl1
7	22	66.7	12	9 US-10-113-809-1	Sequence 1, Appl1
8	22	66.7	12	10 US-09-150-947B-2	Sequence 2, Appl1
9	22	66.7	13	10 US-09-150-947B-5	Sequence 5, Appl1
10	22	66.7	13	10 US-09-150-947B-6	Sequence 6, Appl1
11	22	66.7	13	10 US-09-150-947B-11	Sequence 11, Appl1
12	22	66.7	14	10 US-09-150-947B-9	Sequence 9, Appl1
13	22	66.7	14	10 US-09-150-947B-10	Sequence 10, Appl1
14	22	66.7	16	10 US-09-150-947B-7	Sequence 7, Appl1
15	22	66.7	26	10 US-09-150-947B-1	Sequence 1, Appl1
16	22	66.7	35	10 US-09-150-947B-8	Sequence 8, Appl1
17	22	66.7	102	9 US-10-047-260-26	Sequence 26, Appl
18	22	66.7	230	9 US-10-002-784A-26	Sequence 26, Appl

20	22	66.7	239	1	US-08-882-431-10	Sequence 10, Appl
21	22	66.7	239	9	US-10-002-784A-10	Sequence 10, Appl
22	22	66.7	239	10	US-09-150-947B-12	Sequence 12, Appl
23	22	66.7	251	1	US-08-882-431-16	Sequence 16, Appl
24	22	66.7	251	8	US-08-973-931A-13	Sequence 13, Appl
25	22	66.7	251	9	US-10-002-784A-16	Sequence 16, Appl
26	22	66.7	251	1	US-08-882-431-6	Sequence 6, Appl1
27	22	66.7	251	1	US-08-882-431-8	Sequence 8, Appl1
28	22	66.7	266	9	US-09-870-759-10	Sequence 10, Appl
29	22	66.7	266	9	US-10-002-784A-6	Sequence 6, Appl1
30	22	66.7	266	9	US-10-002-784A-8	Sequence 8, Appl1
31	22	66.7	266	9	US-10-151-336-8	Sequence 8, Appl1
32	22	66.7	295	10	US-09-815-242-13351	Sequence 13351, A
33	22	66.7	295	10	US-09-815-242-13691	Sequence 13691, A
34	22	66.7	344	9	US-10-201-310-3	Sequence 3, Appl1
35	22	66.7	350	9	US-09-972-733-38	Sequence 38, Appl
36	22	66.7	468	9	US-10-002-784A-27	Sequence 27, Appl
37	22	66.7	659	9	US-10-102-627-74	Sequence 74, Appl
38	22	66.7	922	10	US-09-879-228-2	Sequence 2, Appl1
39	22	63.6	12	9	US-10-113-809-2	Sequence 2, Appl1
40	21	63.6	72	9	US-10-144-929-189	Sequence 189, Appl
41	21	63.6	177	9	US-10-092-849-5	Sequence 5, Appl1
42	21	63.6	177	10	US-09-730-617-95	Sequence 95, Appl
43	21	63.6	190	9	US-09-738-626-4637	Sequence 4637, Appl
44	21	63.6	203	9	US-09-900-766-5	Sequence 5, Appl1
45	21	63.6	217	9	US-09-900-766-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-864-761-43487
Sequence 43487, Application US/09864761
Patient No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Neomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43487
LENGTH: 29
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006299.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66
OTHER INFORMATION: EST_HUMAN HIT: AV703706.1, EVALU6 6.00e+00
US-09-864-761-43487

Query Match 69.7%; Score 23; DB 10; Length 29;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | |
DB 10 KALSTGQELD 19

RESULT 2
US-08-882-431-14
Sequence 14, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266

TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match 69.7%; Score 23; DB 1; Length 266;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | |
DB 178 KKSVTQQELD 187

RESULT 3
US-09-870-759-12
Sequence 12, Application US/09870759
Patent No. US20020177531A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-12

Query Match 69.7%; Score 23; DB 9; Length 266;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | |
DB 178 KKSVTQQELD 187

RESULT 4
US-10-002-784A-14
Sequence 14, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 14
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 69.7%; Score 23; DB 9; Length 266;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | |

Db 178 KKVTAEELD 187

RESULT 5

US-09-150-947B-3

; Sequence 3, Application US/09150947B
; Patent No. US20020028211A1

; GENERAL INFORMATION:

; APPLICANT: Kaempfer, Raymond

; APPLICANT: Arad, Gila

; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS

; FILE REFERENCE: A31967-PCT-USA-A

; CURRENT APPLICATION NUMBER: US/09/150,947B

; CURRENT FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: PCT/IL97/00438

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: ISRAEL 119938

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-150-947B-3

Query Match 66.7%; Score 22; DB 10; Length 10;

Best Local Similarity 50.0%; Pred. No. 4.2;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12

Db 1 KKVTAEELD 10

RESULT 6

US-09-150-947B-4

; Sequence 4, Application US/09150947B

; Patent No. US20020028211A1

; GENERAL INFORMATION:

; APPLICANT: Kaempfer, Raymond

; APPLICANT: Arad, Gila

; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS

; FILE REFERENCE: A31967-PCT-USA-A

; CURRENT APPLICATION NUMBER: US/09/150,947B

; CURRENT FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: PCT/IL97/00438

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: ISRAEL 119938

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-150-947B-4

Query Match 66.7%; Score 22; DB 10; Length 10;

Best Local Similarity 50.0%; Pred. No. 4.2;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12

Db 1 KKVTAEELD 10

RESULT 7

US-10-113-809-1

; Sequence 1, Application US/10113809

; Patent No. US20020177573A1

; GENERAL INFORMATION:

; APPLICANT: Masche, Hans, E.

; TITLE OF INVENTION: EXOTOXIN-LIGAND

; FILE REFERENCE: MBP-011XX

; CURRENT APPLICATION NUMBER: US/10/113,809

; CURRENT FILING DATE: 2002-03-29

; PRIOR APPLICATION NUMBER: 101 16 042.9-41

; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Bacterial Toxin Binding Ligand

US-10-113-809-1

Query Match 66.7%; Score 22; DB 9; Length 12;

Best Local Similarity 50.0%; Pred. No. 5.1;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12

Db 3 KKVTAEELD 12

RESULT 8

US-10-113-809-4

; Sequence 4, Application US/10113809

; Patent No. US20020177573A1

; GENERAL INFORMATION:

; APPLICANT: Masche, Hans, E.

; TITLE OF INVENTION: EXOTOXIN-LIGAND

; FILE REFERENCE: MBP-011XX

; CURRENT APPLICATION NUMBER: US/10/113,809

; CURRENT FILING DATE: 2002-03-29

; PRIOR APPLICATION NUMBER: 101 16 042.9-41

; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Bacterial Toxin Binding Ligand

US-10-113-809-4

Query Match 66.7%; Score 22; DB 9; Length 12;

Best Local Similarity 50.0%; Pred. No. 5.1;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12

Db 3 KKVTAEELD 12

RESULT 9

US-09-150-947B-2

; Sequence 2, Application US/09150947B

; Patent No. US20020028211A1

; GENERAL INFORMATION:

; APPLICANT: Kaempfer, Raymond

; APPLICANT: Arad, Gila

; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS

; FILE REFERENCE: A31967-PCT-USA-A

; CURRENT APPLICATION NUMBER: US/09/150,947B

; CURRENT FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: PCT/IL97/00438

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: ISRAEL 119938

PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 12
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-150-947B-2

Query Match 66.7%; Score 22; DB 10; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 4 KKRATVQELD 13

RESULT 10
US-09-150-947B-5
Sequence 5, Application US/09150947B
Patent No. US20020028211A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Atad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 13
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: LIPID
LOCATION: (1)...(1)
OTHER INFORMATION: N-lauryl cysteine residue
US-09-150-947B-5

Query Match 66.7%; Score 22; DB 10; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 4 KKRATVQELD 13

RESULT 11
US-09-150-947B-6
Sequence 6, Application US/09150947B
Patent No. US20020028211A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Atad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 6
LENGTH: 13
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: LIPID
LOCATION: (1)...(1)
OTHER INFORMATION: N-lauryl cysteine residue
US-09-150-947B-6

Query Match 66.7%; Score 22; DB 10; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 4 KKRATVQELD 13

RESULT 12
US-09-150-947B-11
Sequence 11, Application US/09150947B
Patent No. US20020028211A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Atad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 13
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: ACETYLATION
LOCATION: (1)...(1)
OTHER INFORMATION: N-acetyl group
NAME/KEY: MOD.RES
LOCATION: (13)...(13)
OTHER INFORMATION: D-alanine
US-09-150-947B-11

Query Match 66.7%; Score 22; DB 10; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 4 KKRATVQELD 13

RESULT 13
US-09-150-947B-9
Sequence 9, Application US/09150947B
Patent No. US20020028211A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Atad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30

PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 14
TYPE: PRF
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: DISULFID
LOCATION: (1)...(1)
NAME/KEY: DISULFID
LOCATION: (14)...(14)
US-09-150-947B-9

Query Match 66.7%; Score 22; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 6;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 4 KKKATVQELD 13

RESULT 14
US-09-150-947B-10
Sequence 10, Application US/09150947B
Patent No. US2002002821A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Arad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 14
TYPE: PRF
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: D-alanine
NAME/KEY: MOD_RES
LOCATION: (14)...(14)
OTHER INFORMATION: D-alanine
US-09-150-947B-10

Query Match 66.7%; Score 22; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 6;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 4 KKKATVQELD 13

RESULT 15
US-09-150-947B-7
Sequence 7, Application US/09150947B
Patent No. US2002002821A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Arad, Gila
TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
TITLE OF INVENTION: ANTAGONISTS AND VACCINES

FILE REFERENCE: A31967-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/150,947B
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 16
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-09-150-947B-7

Query Match 66.7%; Score 22; DB 10; Length 16;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 3 KKKATVQELD 12

Search completed: June 5, 2003, 15:49:05
Job time: 14.5455 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:24:01 ; Search time 11.8182 Seconds
(without alignments)
97.613 Million cell updates/sec

Title: US-09-150-947F-16
Perfect score: 33
Sequence: 1 XXXXXXTXQEXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	24	72.7	549	2 E86337	hypothetical prote
2	24	72.7	602	1 RRMZP3	polymerase-associ
3	24	72.7	603	1 RRMZP5	polymerase-associ
4	24	72.7	604	1 RRMZP4	polymerase-associ
5	23	69.7	266	1 ENSAC1	enterotoxin C-1 pr
6	23	69.7	266	2 A60114	enterotoxin C-2 pr
7	23	69.7	266	2 S11885	enterotoxin C3 - S
8	23	69.7	565	2 A87694	ribosomal protein
9	23	69.7	566	2 AB3061	30S ribosomal prot
10	23	69.7	568	1 R3ZRL1	ribosomal protein
11	23	69.7	572	2 E98225	30S ribosomal prot
12	23	69.7	586	1 ORXLE	estrogen receptor
13	23	69.7	3212	2 T24692	hypothetical prote
14	22	66.7	102	2 S74843	hypothetical prote
15	22	66.7	136	2 A89969	enterotoxin YEMT2
16	22	66.7	184	2 F86681	prophage pil prote
17	22	66.7	236	2 S18789	exotoxin A precurs
18	22	66.7	236	2 S18786	exotoxin type A pr
19	22	66.7	236	2 S18783	exotoxin type A pr
20	22	66.7	239	2 D89969	enterotoxin SEM 11
21	22	66.7	240	2 G89991	extracellular ente
22	22	66.7	242	2 C89969	extracellular ente
23	22	66.7	247	2 T22535	hypothetical prote
24	22	66.7	251	2 S29659	exotoxin type A pr
25	22	66.7	251	1 QOECF	replication initia
26	22	66.7	258	2 H89968	enterotoxin Sen 11
27	22	66.7	260	2 E89969	enterotoxin Sen 11
28	22	66.7	266	1 ENSAB6	enterotoxin B prec
29	22	66.7	295	2 D95107	hypothetical prote

30	22	66.7	295	2 F97975	hypothetical prote
31	22	66.7	332	1 DEBYG2	glyceralddehyde-3-P
32	22	66.7	333	2 JCS787	ribonuclease H (EC
33	22	66.7	356	2 T38408	hypothetical prote
34	22	66.7	520	2 G71647	hypothetical prote
35	22	66.7	523	2 F97865	hypothetical prote
36	22	66.7	672	2 F71424	hypothetical prote
37	22	66.7	835	2 T05259	hypothetical prote
38	22	66.7	886	2 T39229	probable disease r
39	22	66.7	922	2 T37292	hypothetical prote
40	22	66.7	946	2 A84133	DNA ligase (ATP) (
41	22	66.7	1146	2 A84136	hypothetical prote
42	22	66.7	1200	2 S77524	hypothetical prote
43	22	66.7	1314	2 A85176	chromosome segrega
44	22	66.7	1327	2 D70759	hypothetical prote
45	22	66.7	1738	2 T14867	probable ctsb prot
					interaptin - slime

ALIGNMENTS

RESULT 1

E86337 hypothetical protein F14010.3 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86337

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurco, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shun, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86337

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-549 <STO>

A:Cross-references: GB:AE005172; NID:95558589; PIDN:AAF8152.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 72.7% Score 24; DB 2; Length 549;
Best Local Similarity 50.0% Pred. No. 62;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 XXXXXQEXD 12
Db 27 KISTGTGEND 36

RESULT 2

RRMZP3 polymerase-associated nucleocapsid phosphoprotein - parainfluenza virus type 3 (strai

C:Species: parainfluenza virus type 3
A:Note: host Homo sapiens (man)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Jul-1997

C:Accession: A27010
R:SP19gs, M.K.; Collins, P.L.
J. Gen. Virol. 67, 2705-2719, 1986

A:Title: Sequence analysis of the P and C protein genes of human parainfluenza virus
A:Reference number: A92793; MUID:87085488; PMID:3025346
A:Accession: A27010

A:Molecule type: mRNA

A:Residues: 1-602 <SPR>

C:Comment: This protein may be a component of the active polymerase.

C:Genetics:

A:Gene: P
C:Superfamily: parainfluenza virus polymerase-associated nucleocapsid phosphoprotein

C:Keywords: nucleocapsid; phosphoprotein

Query Match 72.7%; Score 24; DB 1; Length 602;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 226 KSSSTHQEDD 235

RESULT 3

RRNZP5

polymerase-associated nucleocapsid phosphoprotein (version 2) - parainfluenza virus type C:Species: parainfluenza virus type 3

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 24-Jul-1997

C:Accession: A26896

R:Gallinetti, M.S.; Mink, M.A.; Lambert, D.M.; Wechsler, S.L.; Pons, M.W.

Virology 155, 46-60, 1986

A:Title: Molecular cloning and sequence analysis of the human parainfluenza 3 virus mRNA

A:Reference number: A94348; PMID:87044104; PMID:3022477

A:Accession: A26896

A:Molecule type: mRNA

A:Residues: 1-603 <GAL>

C:Comment: The RNA sequence was obtained from GenBank, release 52.0.

C:Genetics:

A:Gene: P

C:Superfamily: parainfluenza virus polymerase-associated nucleocapsid phosphoprotein

C:Keywords: nucleocapsid; phosphoprotein

Query Match 72.7%; Score 24; DB 1; Length 603;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 226 KSSSTHQEDD 235

RESULT 4

RRNZP4

polymerase-associated nucleocapsid phosphoprotein (version 1) - parainfluenza virus type C:Species: parainfluenza virus type 3

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Jul-1997

C:Accession: A94355; A24189

R:Liuk, D.; Sanchez, A.; Banerjee, A.K.

Virology 156, 193-194, 1987

A:Reference number: A94355

A:Contents: extractum

A:Accession: A94355

A:Molecule type: mRNA

A:Residues: 1-604 <LDU>

A:Cross-references: GB:M14890

R:Liuk, D.; Sanchez, A.; Banerjee, A.K.

Virology 153, 318-325, 1986

A:Title: Messenger RNA encoding the phosphoprotein (P) gene of human parainfluenza virus

A:Reference number: A94343; PMID:86291173; PMID:3016995

A:Accession: A24189

A:Molecule type: mRNA

A:Residues: 1-603, 'AKDQIKKTPNK' <LDU>

A:Note: this sequence has been corrected in reference A94355

C:Comment: This protein may be a component of the active polymerase.

C:Genetics:

A:Gene: P

C:Superfamily: parainfluenza virus polymerase-associated nucleocapsid phosphoprotein

C:Keywords: nucleocapsid; phosphoprotein

Query Match 72.7%; Score 24; DB 1; Length 604;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 226 KSSSTHQEDD 235

RESULT 5

ENSAC1

enterotoxin C-1 precursor - Staphylococcus aureus C:Species: Staphylococcus aureus

C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999

C:Accession: S06356; A01816

R:Bohach, G.A.; Schlievert, P.M.

Mol. Gen. Genet. 209, 15-20, 1987

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatednes

A:Reference number: S06356; PMID:88038352; PMID:2823067

A:Accession: S06356

A:Molecule type: DNA

A:Residues: 1-266 <BOH>

A:Cross-references: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567

R:Schmidt, J.J.; Spero, L.

J. Biol. Chem. 258, 6300-6306, 1983

A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.

A:Reference number: A01816; PMID:83213327; PMID:6189824

A:Accession: A01816

A:Molecule type: protein

A:Residues: 28-75, 'IL', '78-176, 'N', '178-266 <SCH>

C:Genetics:

A:Gene: entC1

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-266/Product: enterotoxin C-1 #status experimental <MAT>

F:120-137/Disulfide bonds: #status experimental

Query Match 69.7%; Score 23; DB 1; Length 266;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
| | | | |
Db 178 KKSVTQEDD 187

RESULT 6

A60114

enterotoxin C-2 precursor - Staphylococcus aureus

N:Alternate names: enterotoxin C-3 precursor

C:Species: Staphylococcus aureus

C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999

C:Accession: A60114; B60114; A33866

R:Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2252, 1989

A:Title: Conservation of the biologically active portions of staphylococcal enterotox

A:Reference number: A60114; PMID:8927549; PMID:2543637

A:Accession: A60114

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-266 <BOH>

A:Accession: B60114

A:Molecule type: protein

A:Residues: 28-66 <BOH2>

R:Couch, J.L.; Betley, M.J.

J. Bacteriol. 171, 4507-4510, 1989

A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests

A:Reference number: A33866; PMID:89327174; PMID:2473979

A:Accession: A33866

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-266 <COO>

A:Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004

C:Genetics:

A:Gene: entC2

C;Superfamily: enterotoxin B
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 69.7%; Score 23; DB 2; Length 266;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 178 KKSXTAQEED 187

RESULT 7

S11885
enterotoxin C3 - Staphylococcus aureus

C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C;Accession: S11885
R;Hovde, C.J.; Hackelt, S.P.; Bohach, G.A.

Mol. Gen. Genet. 220, 329-333, 1990

A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison

A;Reference number: S11885; MIMD:90220508; PMID:2325627

A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <NOV>
A;Cross-references: GB:X51661; NID:q46570; PIDN:CAA35972.1; PID:q46571
C;Superfamily: enterotoxin B

Query Match 69.7%; Score 23; DB 2; Length 266;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 178 KKSXTAQEED 187

RESULT 8

A87694
ribosomal protein S1 [Imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

R;Accession: A87694
C;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolenko, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MIMD:21173698; PMID:11259647

A;Accession: A87694
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <STO>
A;Cross-references: GB:AE005673; NID:g13425331; PIDN:AAK25549.1; GSPDB:GN00148
C;Genetics: CC3587
A;Gene: CC3587
C;Superfamily: Escherichia coli ribosomal protein S1

Query Match 69.7%; Score 23; DB 2; Length 565;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 326 KIVSTQSEVD 335

AB3061
30S ribosomal protein S1 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)

RESULT 9
AB3061
30S ribosomal protein S1 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB3061
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.

A;Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AB3061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-566 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAU4904.1; PID:g17742555; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics: rpsA
A;Gene: rpsA
A;Map position: linear chromosome
C;Superfamily: Escherichia coli ribosomal protein S1

Query Match 69.7%; Score 23; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 326 KIVSTQSEVD 335

RESULT 10
R32R1
ribosomal protein S1 - Rhizobium meliloti

C;Species: Rhizobium meliloti
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

C;Accession: S01055
R;Schneider, J.; Thamm, S.; Lutz, R.; Hussain, A.; Faist, G.; Dobrinski, B.

Nucleic Acids Res. 16, 3075-3089, 1988

A;Title: Cloning and characterization of a gene from Rhizobium meliloti 2011 coding

A;Reference number: S01055; MIMD:88217521; PMID:3368316

A;Accession: S01055
A;Molecule type: DNA
A;Residues: 1-568 <SCCH>
A;Cross-references: EMBL:X07528; NID:q46338; PIDN:CAA30404.1; PID:q46339
A;Note: the sequence from Fig. 5 is inconsistent with that from Fig. 4 in having 565-
C;Genetics: rpsA
A;Gene: rpsA
C;Superfamily: Escherichia coli ribosomal protein S1
C;Keywords: duplication; protein biosynthesis; ribosome; RNA binding
F:196-453/Domain: RNA binding #status predicted <RNA>
F:196-279,280-366,367-453/Region: duplication

Query Match 69.7%; Score 23; DB 1; Length 568;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 326 KIVSTQSEVD 335

RESULT 11
E98225
30S ribosomal protein S1 [Imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002

C;Accession: E98225
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A;Reference number: A97359; PMID:11743194

A;Accession: E98225

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-572 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK9327.1; PID:g15159167; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_1496
A:Map position: linear chromosome
C:Superfamily: Escherichia coli ribosomal protein S1

Query Match 69.7%; Score 23; DB 2; Length 572;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 332 KILSTQGEVD 341

RESULT 12

ORXLE

estrogen receptor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 15-Jun-1996

C:Accession: M40907
R:Weller, I.J.; Lew, D.; Shapiro, D.J.
MOL. Endocrinol. 1, 355-362, 1987

A:Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian re
A:Reference number: M40907; MUID:90331927; PMID:3274894
A:Accession: M40907
A:Molecule type: mRNA

A:Residues: 1-586 <WEI>
A:Cross-references: GB:L20735

C:Comment: The steroid hormones and their receptors are involved in the regulation of eu
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F:1-174/Domain: amino-terminal <NH2>
F:175-266/Domain: DNA binding #status predicted <DNA>
F:178-448/Domain: erba transforming protein homology <ERBA>
F:178-201/Region: zinc finger CCCC motif
F:214-237/Region: zinc finger CCCC motif
F:251-266/Region: nuclear location signal
F:292-544/Domain: steroid binding #status predicted <STR>
F:180,183,197,200/Binding site: zinc (Cys) #status predicted
F:215,222,232,235/Binding site: zinc (Cys) #status predicted
F:231/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 69.7%; Score 23; DB 1; Length 586;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 545 KDKTTQGEVD 554

RESULT 13

T24692

hypothetical protein T08G11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T24692
R:Dobson, R.
submitted to the EMBL Data Library, September 1996

A:Reference number: 219925
A:Accession: T24692
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-3212 <WIL>
A:Cross-references: EMBL:T80220; PIDN:CA802304.1; GSPDB:GN00019; CESP:T08G11.1

A:Experimental source: clone T08G11
C:Genetics:

A:Gene: CESP:T08G11.1
A:Map position: 1
A:Introns: 34/1; 149/3; 182/3; 527/2; 766/1; 1070/3; 1769/3; 1834/3; 2070/2; 2210/3;

Query Match 69.7%; Score 23; DB 2; Length 3212;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 2264 KSVTTSQEND 2273

RESULT 14

S74843

hypothetical protein S110846 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S74843
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
5.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74843
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <KAN>
A:Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BA17804.1; PID:g101

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
Query Match 66.7%; Score 22; DB 2; Length 102;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 72 KKKTKQGEVD 81

RESULT 15

A89969

enterotoxin YENT2 [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: A89969
R:Kuruda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: GB:BA000018; PID:g13701619; PIDN:BB42912.1; GSPDB:GN00149

A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match 66.7%; Score 22; DB 2; Length 136;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 50 KKNITQGEVD 59

Search completed: June 5, 2003, 15:34:00

Job time : 11.8182 secs



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:34:07 ; Search time 7.81818 Seconds

(without alignments)
63.661 Million cell updates/sec

Title: US-09-150-947F-16

Perfect score: 33

Sequence: 1 XXXXXXXXQEXD 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.7	60.4	1	RRP_P13H4	P06162 human para
2	69.7	26.6	1	ETC1_STRAU	P01553 staphylococ
3	69.7	26.6	1	ETC2_STRAU	P34071 staphylococ
4	69.7	26.6	1	ETC3_STRAU	P23313 staphylococ
5	69.7	56.8	1	ESR1_RHIME	P14129 rhizobium m
6	69.7	56.8	1	ESR1_XENLA	P81559 xenopus lae
7	66.7	25.1	1	REEL_ECOLI	P03856 escherichia
8	66.7	25.1	1	SPER_STRPY	P08095 streptococ
9	66.7	26.6	1	ETXB_STRAU	P01552 staphylococ
10	66.7	33.1	1	GP3_YEAST	P00359 saccharomyc
11	66.7	35.0	1	DKK3_CHICK	P00839 gallus gall
12	66.7	35.6	1	YDGC_SCHPO	O10498 schizosacch
13	66.7	52.0	1	Y855_RICPR	O9ZC45 rickettsia
14	66.7	71.2	1	ARS2_CAEEL	O96615 caenorhabdl
15	66.7	88.6	1	YE86_SCHPO	O14302 schizosacch
16	66.7	92.2	1	DNL3_HUMAN	P49192 homo sapien
17	66.7	101.5	1	DNL3_MOUSE	P97386 mus musculi
18	66.7	132.7	1	YK06_MYCTU	O10850 mycobacteri
19	63.6	17.6	1	YR59_LISMO	O8Y583 listeria mo
20	63.6	17.7	1	GL1_HORSE	O18899 equus cabal
21	63.6	22.8	1	GL1_ARATH	P27900 arabidopsis
22	63.6	23.4	1	SPG_STRPY	O9X5C7 streptococ
23	63.6	23.5	1	SPEC_STRPY	P13380 streptococ
24	63.6	23.6	1	SPH_STRPY	O9X5C8 streptococ
25	63.6	25.7	1	ETXA_STRAU	P13163 staphylococ
26	63.6	25.7	1	ETXE_STRAU	P12993 staphylococ
27	63.6	25.8	1	ETXD_STRAU	P20723 staphylococ
28	63.6	25.8	1	ETYG_STRAU	O85382 staphylococ
29	63.6	27.6	1	PYGL_SYNEL	P50039 synecchococ
30	63.6	28.3	1	YJ81_YEAST	P47148 saccharomyc
31	63.6	35.1	1	PEXE_PICAN	P78123 picchia angu
32	63.6	37.5	1	NP14_HUMAN	O99733 homo sapien
33	63.6	38.5	1	TGT_ZYMAN	P28720 zymomonas m

34	21	63.6	461	1	DISK_MOUSE	O61466 mus musculu
35	21	63.6	480	1	SYF_MYCLE	O92517 mycobacteri
36	21	63.6	554	1	NBL4_MOUSE	P52963 mus musculu
37	21	63.6	684	1	FLID_HELPJ	O92191 helicobacte
38	21	63.6	684	1	FLID_HELPJ	P96786 helicobacte
39	21	63.6	727	1	GPKM_HUMAN	P43304 homo sapien
40	21	63.6	727	1	GPKM_MOUSE	O64521 mus musculu
41	21	63.6	899	1	ANDR_MOUSE	P19091 mus musculu
42	21	63.6	904	1	NIA1_TOBAC	P11605 nicotiana t
43	21	63.6	904	1	NIA2_TOBAC	P08509 nicotiana t
44	21	63.6	1184	1	XMS2_DROME	O93399 drosophila
45	21	63.6	1305	1	GAK_RAT	P97874 ratius norv

ALIGNMENTS

```

RESULT 1
ID      RRP_P13H4      STANDARD;      PRT;      604 AA.
AC      P06162;
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      01-AUG-1988 (Rel. 08, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
DE      phosphoprotein).
GN      P.
OS      Human parainfluenza 3 virus (strain NIH 47885).
OC      Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC      Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX      NCBI_TaxID=11217;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86291173; PubMed=3016995;
RA      Luk D., Sanchez A., Banerjee A.K.;
RT      "Messenger RNA encoding the phosphoprotein (P) gene of human
RT      parainfluenza virus 3 is bicistronic.";
RL      Virology 153:318-325(1986).
RN      [2]
RP      REVISIONS.
RA      Luk D., Sanchez A., Banerjee A.K.;
RL      Virology 156:193-194(1987).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87044104; PubMed=3022477;
RA      Gallus M.S., Mink M.A., Lambert D.M., Wechsler S.L., Pons W.M.;
RT      "Molecular cloning and sequence analysis of the human parainfluenza 3
RT      virus mRNA encoding the P and C proteins.";
RL      Virology 155:46-60(1986).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87085488; PubMed=3025346;
RA      Spriggs M.K., Collins P.L.;
RT      "Sequence analysis of the P and C protein genes of human
RT      parainfluenza virus type 3: patterns of amino acid sequence homology
RT      among paramyxovirus proteins.";
RL      J. Gen. Virol. 67:2705-2719(1986).
CC      -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC      POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC      -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC      (RNA)(N).
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
DR      EMBL: M14890; AAA46866.1; ALT_SEQ.
DR      EMBL: X04721; CAA28429.1; -.
DR      EMBL: M14932; AAA66818.1; -.

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DR EMBL: D10029; BAA00921.1; ALT_SEQ.
 DR PIR: A27010; RKNZP3.
 DR PIR: A24189; RKNZP4.
 DR PIR: A26896; RKNZP5.
 DR InterPro: IPR002693; Paramyxo_P.
 DR Pfam: PF01806; Paramyxo_P.1.
 KW Transferrase; RNA-directed RNA polymerase; Nucleocapsid;
 KM Phosphorylation.
 FT CONFLICT 198 198 P -> N (IN REF. 4).
 FT CONFLICT 243 243 MISSING (IN REF. 3 AND 4).
 FT CONFLICT 244 244 MISSING (IN REF. 4).
 FT CONFLICT 316 316 O -> R (IN REF. 3).
 FT CONFLICT 584 584 C -> S (IN REF. 4).
 SQ SEQUENCE 604 AA; 67661 MW; D2E06EF47027D0BD CRC64;
 Query Match 72.7%; Score 24; DB 1; Length 604;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 3 KXXXTXQEXD 12
 Db 226 KKSSTHQEDD 235
 RESULT 2
 ETC2_STAAU STANDARD; PRT; 266 AA.
 ID ETC2_STAAU
 AC P01553;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-1 precursor (SEC1).
 GN EMTCL.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88038352; PubMed=2823067;
 RA Bohach G.A., Schlievert P.M.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
 RL Mol. Gen. Genet. 209:15-20(1987).
 RN [2]
 RP SEQUENCE OF 28-266.
 RX MEDLINE=83213327; PubMed=6189824;
 RA Schmidt J.J., Spero L.;
 RT "The complete amino acid sequence of staphylococcal enterotoxin C1";
 RL J. Biol. Chem. 258:6300-6306(1983).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 CC EMBL: X05815; CAA29260.1; -
 DR PIR: A01816; ENSAC1.
 DR PIR: S06356; S06356.
 DR HSSP: P34071; 1SE2.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
 FT DISULFID 120 137
 FT CONFLICT 177 177 D -> N (IN REF. 2).
 SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A898653B CRC64;
 Query Match 69.7%; Score 23; DB 1; Length 266;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 3 KXXXTXQEXD 12
 Db 178 KKSVAQELD 187
 RESULT 3
 ETC2_STAAU STANDARD; PRT; 266 AA.
 ID ETC2_STAAU
 AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN EMTCL.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 RL Enterotoxin C1 and C2";
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RL Staphylococcus aureus reveals a zinc-binding site";
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RL enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RL enterotoxins A and C2 reveals remarkable similarity and
 RL dissimilarity";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC
 CC PIR: A60114; A60114.
 DR PDB: 1STE; 23-DEC-96.
 DR PDB: 1SE2; 08-MAR-96.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

```

DR PROSITE: PS00278; STAPH_STREP_TOXIN.2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; zinc;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFD 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; 8407EB18536FAC08 CRC64;
OY 3 KXXXTXGEXD 12
Db 178 KRSVTAQELD 187

RESULT 4
ETC3_STAM
ID ETC3_STAM STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN EMTCS OR SAV2009 OR SA1817.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcu.
OX NCBI_TaxID=158878, 158879, 1280;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699, and N315;
RC MEDLINE=21311952; PubMed=1418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ilan J.-O., Ito T.,
RA Karamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mutant-ii Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RT Lancet 357:1225-1240(2001).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=90220508; PubMed=2325627;
RX Howde C.J., Hackett S.P., Bohach G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RT Mol. Gen. Genet. 220:329-333(1990).
RL [3]
RN X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
RP MEDLINE=97064178; PubMed=8906797;
RX Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffer C.V.,
RA Schlievert P.M., Karjalainen K., Maruza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen".
RL Nature 384:188-192(1996).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: AP00364; BAB58171.1; -
DR EMBL: AP003135; BAB43097.1; -
DR EMBL: X51661; CA35972.1; -.
DR PIR: S11885; S11885.
DR PDB: 1JCK; 12-NOV-97.
DR InterPro: IPR001961; Strep/Strep_toxin.
DR Pfam: PF01123; Strep_stp_toxin; 1.
DR Pfam: PF02876; Strep_stp_tox_C; 1.
DR PRINTS: PR00279; BACTR_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
KW Complete proteome.
FT SIGNAL 1
FT CHAIN 28 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FCA59 CRC64;

OY 3 KXXXTQXEXD 12
Db 178 KKVTAQELD 187

RESULT 5
RSL_RHIME
ID RSL_RHIME STANDARD: PRT; 568 AA.
AC P14129;
DT 01-JAN-1990 (Rel. 13, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S1
GN RPSA OR R00255 OR SMC00335.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / S047;
RX MEDLINE=86217521; PubMed=3368316;
RA Schmier J., Thamm S., Lutz R., Hussain A., Falst G.,
RA Dobrinski B.;
RT "Cloning and characterization of a gene from Rhizobium meliloti 2011
RT coding for ribosomal protein S1";
RL Nucleic Acids Res. 16:3075-3089(1988).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Goulet T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puenher A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gilbert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 6 SI MOTIF DOMAINS.
CC -----

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DR EMBL; X07528; CAA30404.1; -
 DR EMBL; AL591783; CAC41692.1; -
 DR PIR; S01055; R3ZRL.
 DR HSSP; P05055; ISRO.
 DR InterPro; IPR000110; Ribosomal_S1.
 DR InterPro; IPR003029; S1.
 DR Pfam; PF00575; S1; 6.
 DR PRINTS; PR00681; RIBOSOMAL_S1.
 DR SMART; SM00316; S1; 6.
 DR TIGRfam; TIGR00717; rpsa; 1.
 DR PROSITE; PS50126; S1; 6.
 KW Ribosomal protein; Repeat; RNA-binding; Complete proteome.
 FT DOMAIN 27 93 S1 MOTIF 1.
 FT DOMAIN 111 177 S1 MOTIF 2.
 FT DOMAIN 198 266 S1 MOTIF 3.
 FT DOMAIN 283 353 S1 MOTIF 4.
 FT DOMAIN 370 440 S1 MOTIF 5.
 FT DOMAIN 459 530 S1 MOTIF 6.
 FT CONFLICT 88 A -> R (IN REF. 1).
 FT CONFLICT 153 162 LMHPQPEI -> ADAQPALRN (IN REF. 1).
 FT CONFLICT 235 235 N -> K (IN REF. 1).
 FT CONFLICT 241 241 L -> O (IN REF. 1).
 FT CONFLICT 551 A -> R (IN REF. 1).
 FT SEQUENCE 568 AA; 62640 MW; A80858204273A7B8 CRC64;

Query Match 69.7%; Score 23; DB 1; Length 568;
 Best Local Similarity 50.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 | | | | |
 DB 326 KILSTQEQVD 335

RESULT 6
 ID ESRL_XENLA STANDARD; PRT; 586 AA.
 AC P81559;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
 GN ESR1 OR NR3A1 OR ESR.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 CC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90331927; PubMed=1274894;
 RA Weller I.J., Lew D., Shapiro D.J.;
 RT "The Xenopus laevis estrogen receptor: sequence homology with human
 RT and avian receptors and identification of multiple estrogen receptor
 RT messenger ribonucleic acids.";
 RL Mol. Endocrinol. 1:355-362(1987).
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED
 CC IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
 CC CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -1- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 CC BETA (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

NR3 SUBFAMILY.

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DR EMBL; L20735; -; NOT_ANNOTATED_CDS.
 DR HSSP; P03372; HRCQ.
 DR TRANSFAC; T00263; -
 DR InterPro; IPR000536; Hormone_rec_11g.
 DR InterPro; IPR001292; Oestrgn_receptor.
 DR InterPro; IPR001723; Sthrmn_receptor.
 DR InterPro; IPR001628; ZnF_Casteroid.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR Pfam; PF02159; Oest_rec; 1.
 DR PRINTS; PR00398; STRDHOMONER.
 DR PRINTS; PR00447; STROIDFINGER.
 DR PRODOM; PD000035; ZnF_Casteroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; ZnF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 FT ZINC-FINGER; Steroid-binding.
 FT DOMAIN 1 179 MODULATING.
 FT DNA_BIND 180 245 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 180 200 C4-TYPE.
 FT ZN_FING 216 240 C4-TYPE.
 FT DOMAIN 246 302 HINGE.
 FT DOMAIN 303 586 STEROID-BINDING.
 FT SEQUENCE 586 AA; 66080 MW; 0EDC77EBD06F08BF CRC64;

Query Match 69.7%; Score 23; DB 1; Length 586;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 | | | | |
 DB 545 KDKTTQEQED 554

RESULT 7
 ID REEL_ECOLI STANDARD; PRT; 251 AA.
 AC P03856; P08969;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Replication initiation protein (RIP protein) (protein E) (F4 protein).
 GN REP OR REP OR E.
 OS Escherichia coli.
 OX Escherichia coli.
 OX Plasmid F.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82051318; PubMed=7028572;
 RA Murotsu T., Matsubara K., Sugisaki H., Takanami M.;
 RT "Nine unique repeating sequences in a region essential for
 RT replication and incompatibility of the mini-F plasmid.";
 RL Gene 15:257-271(1981).
 CC [2]
 RP SEQUENCE FROM N.A.
 RP Eichenlaub R.;
 RA "F plasmid DNA complete mini-F region (F coordinates 40,301F to
 RT 49,869F).";
 RL Submitted (Aug-1986) to the EMBL/Genbank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / CR63;
 RA Shimizu H., Saitoh Y., Suda Y., Uehara K., Sampel G., Mizobuchi K.;
 RT "Complete nucleotide sequence of the F plasmid: its implications for
 RT organization and diversification of F plasmid genomes.";
 RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 211-251 FROM N.A.
 RX MEDLINE-81234554; PubMed-7018695;
 RA Tolun A., Helinski D.R.;
 RT "Direct repeats of the F plasmid *lncC* region express F
 RT incompatibility.";
 RL Cell 24:687-694(1981).
 RN [5]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE-86174346; PubMed-3007930;
 RA Digue-Kochem C., Seidel U., Helsenberg M., Eichenlaub R.;
 RT "The repeated sequences (*lncB*) preceding the protein E gene of
 RT plasmid *mln1-F* are essential for replication.";
 RL Mol. Gen. Genet. 202:132-135(1986).
 RN [6]
 RP SEQUENCE OF 209-251 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-87141188; PubMed-3029390;
 RA Mori H., Kondo A., Ohshima A., Ogura T., Hiraga S.;
 RT "Structure and function of the F plasmid genes essential for
 RT partitioning.";
 RL J. Mol. Biol. 192:1-15(1986).
 CC -1- SIMILARITY: REGIONS OF SIMILARITY WITH REPA PROTEIN OF THE P1
 CC PLASMID, BUT NOT WITH REPLICATION PROTEINS OF OTHER PLASMIDS.
 CC -----
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 CC -----
 DR EMBL: J01724; AAA91062.1; -
 DR EMBL: M12987; AAA24901.1; -
 DR EMBL: AP001918; BA97915.1; -
 DR EMBL: X03410; CAA27146.1; -
 DR EMBL: X04619; CAA28294.1; -
 DR PIR: A04485; QOECF.
 DR PIR: D25783; D25783.
 DR Ecogene: EG40058; repe.
 DR InterPro: IPR000525; Initr_Repr.
 DR Pfam: PF01051; RepB_protein; 1.
 DR Plasmid: DNA replication; Plasmid copy control; Complete proteome.
 SK SEQUENCE 251 AA; 29358 MW; EA2BC265D80158B2 CRC64;

Query Match 66.7%; Score 22; DB 1; Length 251;
 Best Local Similarity 50.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 DB 48 KSDGTQEHND 57

RESULT 8
 SPEA_STRPY STANDARD; PRT; 251 AA.
 AC P08095;
 DT 01-AUG-1988 (rel. 08, Created)
 DT 01-JAN-1990 (rel. 13, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
 DE (SPE A).
 GN SPEA OR SPYMI8_0393.
 OS Streptococcus pyogenes, and
 OS Streptococcus pyogenes (serotype M18).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314, 186103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86166804; PubMed-3514452;
 RA Weeks C.R., Ferretti J.J.;
 RT "Nucleotide sequence of the type A streptococcal exotoxin
 RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
 RT T12.";
 RL Infect. Immun. 52:144-150(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86284313; PubMed-3526093;
 RA Johnson L.P., L'Italian J.J., Schlievert P.M.;
 RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
 RT related to Staphylococcus aureus enterotoxin B.";
 RL Mol. Gen. Genet. 203:354-356(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MGAS8232 / Serotype M18;
 RX MEDLINE-21927593; PubMed-11917108;
 RA Smoot J.C., Barbien K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcilla S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
 RX MEDLINE-99094887; PubMed-9878045;
 RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
 RA O'Brien S.M., Tranter H.S., Acharya K.R.;
 RT "Structural basis for the recognition of superantigen streptococcal
 RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
 RT receptors.";
 RL EMBO J. 18:9-21(1999).
 CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
 CC chain.
 CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 DR EMBL: U40453; AAC48868.1; -
 DR EMBL: X03928; CAA27568.1; -
 DR EMBL: AE009982; AAL97141.1; -
 DR PIR: A26152; A26152.
 DR PIR: S29659; S29659.
 DR PDB: 1B12; 24-NOV-99.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph-Strep_toxin; 1.
 DR Pfam: PF02876; Staph-Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; 3D-structure.
 KM STGNAL 1 30
 FT CHAIN 31 251 EXOTOXIN TYPE A.

DT 15-JUN-2002 (rel. 41, last annotation update)
 DE glyceraldehyde 3-phosphate dehydrogenase 3 (EC 1.2.1.12) (GAPDH 3).
 GN IDH3 OR GPD3 OR YGR192C OR G7576.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 ON NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=80027306; PubMed=385592;
 RA Holland J.P., Holland M.J.,
 RT "The primary structure of a glyceraldehyde-3-phosphate dehydrogenase
 RT gene from *Saccharomyces cerevisiae*.";
 RL J. Biol. Chem. 254:9839-9845(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=S288C;
 RC MEDLINE=95373283; PubMed=7645350;
 RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez M.,
 RA Nombela C.;
 RT "The complete sequence of a 9037 bp DNA fragment of the right arm of
 RT yeast 11:587-591(1995)."
 RL yeast 11:587-591(1995).
 RN [3]
 RP SEQUENCE OF 46-57.
 RC STRAIN=S288C;
 RC MEDLINE=95203288; PubMed=7895733;
 RA Garets J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database.";
 RL Electrophoresis 15:1466-1486(1994).
 RN [4]
 RP PARTIAL SEQUENCE.
 RC STRAIN=ATCC 38531 / Y41, and SKO2N;
 RX MEDLINE=95255188; PubMed=7737086;
 RX Norbeck J., Blomberg A.;
 RT "Gene linkage of two-dimensional polyacrylamide gel electrophoresis
 RT resolved proteins from isogene families in *Saccharomyces cerevisiae*
 RT by microsequencing of in-gel trypsin generated peptides.";
 RL Electrophoresis 16:149-156(1995).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) -> 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE THREE GENES FOR G3PDH IN YEAST.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 CC DEHYDROGENASE FAMILY.
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 CC -----
 DR EMBL: V01300; CAA24607.1; -;
 DR EMBL: V01324; AAA88714.1; -;
 DR EMBL: X82408; CAA57803.1; -;
 DR EMBL: Z72977; CAA97218.1; -;
 DR PIR: A00371; DEBYG2.
 DR HSSP: P06977; 1GAD.
 DR SWISS-2DPAGE: P00359; YEAST.
 DR COMPUYEST-2DPAGE: P00359; -;
 DR SGD: S0003424; TDH3.
 DR InterPro: IPR000173; GAP_dhhydrogenase.
 DR Pfam: PF00044; gpdh.1.
 DR Pfam: PF02800; gpdh.C.1.
 DR PRINTS: PR00078; G3PDHGRNASE.
 DR PROSITE: PS00071; GAPDH; 1.
 KW Glycolysis; Oxidoreductase; NAD; Multigene family.

FT INIT_MET 0 0
 FT BINDING 149 149 GLYCERALDEHYDE 3-PHOSPHATE.
 FT ACT_SITE 176 176 ACTIVATES THOL GROUP DURING CATALYSIS.
 FT CONFLICT 135 135 E -> V (IN REF. 1).
 FT CONFLICT 247 247 N -> D (IN REF. 1).
 FT CONFLICT 328 328 V -> I (IN REF. 1).
 SQ SEQUENCE 331 AA; 35615 MW; CFE994A335C648B5 CRC64;
 Query Match 66.7%; Score 22; DB 1; Length 331;
 Best Local Similarity 50.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXXXTQXEND 12
 Db 69 KRATYQERD 78
 RESULT 11
 DKK3_CHICK STANDARD; PRT; 350 AA.
 AC 090839;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DICKKOPF related protein-3 precursor (Dkk-3) (Dickkopf-3) (Lens fiber
 DE protein CLFEST4).
 GN DKK3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lens fibers;
 RX MEDLINE=96437509; PubMed=8840185;
 RA Sawada K., Agata K., Eguchi G.;
 RT "Characterization of terminally differentiated cell state by
 RT categorizing cDNA clones derived from chicken lens fibers.";
 RL Int. J. Dev. Biol. 40:531-535(1996).
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: secreted (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EYE LENS.
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
 CC -----
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 CC -----
 DR EMBL: D26311; BAA05373.1; -;
 DR HSSP: P25687; 1IMT.
 KW Developmental protein; Signal; Glycoprotein.
 FT SIGNAL 1 29
 FT CHAIN 30 350
 FT DOMAIN 139 187
 FT CARBOHYD 200 277
 FT CARBOHYD 88 88
 FT CARBOHYD 98 98
 FT CARBOHYD 113 113
 FT CARBOHYD 196 196
 FT CARBOHYD 282 282
 SQ SEQUENCE 350 AA; 39208 MW; 57BE7EBD50089DAE CRC64;
 Query Match 66.7%; Score 22; DB 1; Length 350;
 Best Local Similarity 50.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KXXXTQXEND 12
 I I I I I

Db 99 KTVOTHOEID 108

RESULT 12

YDGC_SCHPO

ID YDGC_SCHPO STANDARD: PRT: 356 AA.

AC 010498:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C26F1.12c in chromosome I.

GN SPAC26F1.12c

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA MEDLINE-21848401; PubMed-11859360;

RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squires J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Ritter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volkart G., Aert R., Robben J., Grymponprez B.,

RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambolt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerruti L., Love T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakowski G.V., Ussey D., Barrett B.G., Nurse P.;

RA "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

CC -1 SIMILARITY: TO YEAST HGHI.

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CC EMBL: 273100; CAA97369.1;

DR Hypothetical protein.

KW SEQUENCE 356 AA; 41260 MW; AD1BC71AC134AA1C CRC64;

Query Match 66.7%; Score 22; DB 1; Length 356;

Best Local Similarity 50.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12

DB 178 KYFTTLDYD 187

OY 3 KXXXTXQEXD 12

DB 178 KYFTTLDYD 187

OY 3 KXXXTXQEXD 12

DB 178 KYFTTLDYD 187

OY 3 KXXXTXQEXD 12

DB 178 KYFTTLDYD 187

OY 3 KXXXTXQEXD 12

DB 178 KYFTTLDYD 187

OY 3 KXXXTXQEXD 12

DB 178 KYFTTLDYD 187

OY 3 KXXXTXQEXD 12

AC 092CA5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein RP855.

GN RP855.

OS Rickettsia prowazekii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI_TaxID=782;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Madrid E;

RA MEDLINE-99039499; PubMed-9823893;

RA Anderson S.G.E., Zomorodipour A., Andersson J.O.,

RA Sichert-Bonten T., Alsmark U.C.M., Podowski R.M., Naeisund A.K.,

RA Eriksson A.-S., Winkler H.H., Kurian C.G.;

RA "The genome sequence of Rickettsia prowazekii and the origin of

RA mitochondria.";

RL Nature 396:133-140(1998).

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CC EMBL: AJ235273; CAA15279.1;

DR Hypothetical protein; Transmembrane, Complete proteome.

KW TRANSMEM 337 POTENTIAL.

SQ SEQUENCE 520 AA; 61113 MW; AAB4DBA1E594034 CRC64;

Query Match 66.7%; Score 22; DB 1; Length 520;

Best Local Similarity 50.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

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OY 3 KXXXTXQEXD 12

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DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

OY 3 KXXXTXQEXD 12

DB 374 KYRANQEXD 383

EMBL: AC006627; AAK85459.1;

DR WormPep: E01A2.2; CE20643.

KW Hypothetical protein.
 SQ SEQUENCE 712 AA; 80794 MW; 54B051ADAF547DE CRC64;
 Query Match
 Best Local Similarity 50.0%; Score 22; DB 1; Length 712;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 Db 88 KKFITSQEDD 97

RESULT 15
 YE86_SCHPO
 ID YE86_SCHPO STANDARD; PRT; 886 AA.
 AC 014302;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C9G1.06c in chromosome I.
 GN SPAC9G1.06c.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Wellens I., Vanstreels E., Aert R., Robben J., Grymonprez B.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wandut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: TO YEAST YDL117M.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; Z98763; CAB11490.1; -
 DR HSSP; P29355; ISEM.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR002931; Trnsglucanase_like.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000066; SH3; 1.

DR SMART; SM00326; SH3; 1.
 DR SMART; SM00460; TGC; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Hypothetical protein: SH3 domain.
 FT DOMAIN 6 67 SH3.
 FT POLY-SER.
 SQ SEQUENCE 886 AA; 98262 MW; D0C4879C1882E869 CRC64;
 Query Match
 Best Local Similarity 40.0%; Score 22; DB 1; Length 886;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 Db 220 KSTTSKEDD 229

Search completed: June 5, 2003, 15:56:34
 Job time: 7.81818 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:32:58 ; Search time 34.9091 Seconds
(without alignments)
70.829 Million cell updates/sec

Title: US-09-150-947F-16
Perfect score: 33
Sequence: 1 XXXXXXTXQEXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	72.7	209	09R005	09R95 streptococ
2	24	72.7	209	09LAE1	09LAE1 streptococ
3	24	72.7	209	09LAE0	09LAE0 streptococ
4	24	72.7	209	09LAD9	09LAD9 streptococ
5	24	72.7	209	09LAD8	09LAD8 streptococ
6	24	72.7	209	09LAD7	09LAD7 streptococ
7	24	72.7	209	09LAD6	09LAD6 streptococ
8	24	72.7	209	09LAD5	09LAD5 streptococ
9	24	72.7	209	09LAD4	09LAD4 streptococ
10	24	72.7	209	09LAD3	09LAD3 streptococ
11	24	72.7	209	09LAD2	09LAD2 streptococ
12	24	72.7	209	09LAD1	09LAD1 streptococ
13	24	72.7	209	09LAD0	09LAD0 streptococ
14	24	72.7	209	09LAC9	09LAC9 streptococ
15	24	72.7	209	09LAC8	09LAC8 streptococ
16	24	72.7	209	09LAC7	09LAC7 streptococ

17	24	72.7	209	2	09LAC6	09LAC6 streptococ
18	24	72.7	209	2	09LAC5	09LAC5 streptococ
19	24	72.7	209	2	09LAC4	09LAC4 streptococ
20	24	72.7	209	2	09LAC3	09LAC3 streptococ
21	24	72.7	209	2	09LAC2	09LAC2 streptococ
22	24	72.7	209	2	09LAC1	09LAC1 streptococ
23	24	72.7	209	2	09LAC0	09LAC0 streptococ
24	24	72.7	209	2	09LAC9	09LAC9 streptococ
25	24	72.7	209	2	09LAC8	09LAC8 streptococ
26	24	72.7	209	2	09LAC7	09LAC7 streptococ
27	24	72.7	209	2	09LAC6	09LAC6 streptococ
28	24	72.7	209	2	09LAC5	09LAC5 streptococ
29	24	72.7	209	2	09LAC4	09LAC4 streptococ
30	24	72.7	209	2	09LAC3	09LAC3 streptococ
31	24	72.7	209	2	09LAC2	09LAC2 streptococ
32	24	72.7	209	2	09LAC1	09LAC1 streptococ
33	24	72.7	209	2	09LAC0	09LAC0 streptococ
34	24	72.7	209	2	09LAC9	09LAC9 streptococ
35	24	72.7	209	2	09LAC8	09LAC8 streptococ
36	24	72.7	209	2	09LAC7	09LAC7 streptococ
37	24	72.7	209	2	09LAC6	09LAC6 streptococ
38	24	72.7	209	2	09LAC5	09LAC5 streptococ
39	24	72.7	209	2	09LAC4	09LAC4 streptococ
40	24	72.7	209	2	09LAC3	09LAC3 streptococ
41	24	72.7	209	2	09LAC2	09LAC2 streptococ
42	24	72.7	209	2	09LAC1	09LAC1 streptococ
43	24	72.7	209	2	09LAC0	09LAC0 streptococ
44	24	72.7	209	2	09LAC9	09LAC9 streptococ
45	24	72.7	209	2	09LAC8	09LAC8 streptococ

ALIGNMENTS

RESULT 1
ID 09R005 PRELIMINARY; PRT; 209 AA.
AC 09R005;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin Z 2 (Fragment).
GN SMEZ-2.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1314;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-2035;
RX MEDLINE-99093428; PubMed-9874566;
RA Prof. T. Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
Streptococcus pyogenes."
RL J. Exp. Med. 189:89-102(1999).
DR EMBL: AF086626; AAD52087.1; -.
DR HSSP: P13163; 1SXT.
DR InterPro: IPR001961; Staph/Strep toxin.
DR Pfam: PF01123; Staph-Strep toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;

Query Match 3 XXXXTXQEXD 12
Best local similarity 72.7%; Score 24; DB 2; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 125 KTTVTAEID 134

RESULT 2

09LAE1 PRELIMINARY; PRT; 209 AA.
 ID 09LAE1;
 AC 09LAE1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Mitogenic exotoxin Z-3 (Fragment).
 GN SMEZ-3.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 CC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11681;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RA "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143653; AAF6654.1; -
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Stap/Strep_toxin.
 DR Pfam; PF01123; Stap_Strep_toxin; 1.
 DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 209 AA; 24071 MW; F0ADFCDDIAA87271 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 1 1 1 1 1
 DB 125 KTYVTAQED 134

RESULT 3

09LAE0 PRELIMINARY; PRT; 209 AA.
 ID 09LAE0;
 AC 09LAE0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Mitogenic exotoxin Z-4 (Fragment).
 GN SMEZ-4.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 CC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-9893;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RA "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143654; AAF6655.1; -
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Stap/Strep_toxin.
 DR Pfam; PF01123; Stap_Strep_toxin; 1.
 DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 209 AA; 24108 MW; 67EC279BCC4A8247 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 1 1 1 1 1
 DB 125 KTYVTAQED 134

RESULT 4

09LAD9 PRELIMINARY; PRT; 209 AA.
 ID 09LAD9;
 AC 09LAD9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Mitogenic exotoxin Z-5 (Fragment).
 GN SMEZ-5.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 CC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11244;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RA "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143655; AAF6656.1; -
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Stap/Strep_toxin.
 DR Pfam; PF01123; Stap_Strep_toxin; 1.
 DR Pfam; PF02876; Stap_Strep_toxin_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 209 AA; 24079 MW; 24CA3885469CBB9B CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 1 1 1 1 1
 DB 125 KTYVTAQED 134

RESULT 5

09LAD8 PRELIMINARY; PRT; 209 AA.
 ID 09LAD8;
 AC 09LAD8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Mitogenic exotoxin Z-7 (Fragment).
 GN SMEZ-7.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 CC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11574;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RA "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).

DR EMBL: AF143657; AAF66657.1; -.
 DR HSSP: P13163; ISXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24064 MW; 67E977CD5AA934F7 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 | | | | |
 Db 125 KTTVTAGEID 134

RESULT 6
 Q9LAD7 PRELIMINARY; PRT; 209 AA.
 AC Q9LAD7;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Mitogenic exotoxin z-8 (Fragment).
 GN SMEZ-8.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1/5045;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Mofitt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143658; AAF66658.1; -.
 DR HSSP: P13163; ISXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24091 MW; 7680E9B35513DF28 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 | | | | |
 Db 125 KTTVTAGEID 134

RESULT 7
 Q9LAD6 PRELIMINARY; PRT; 209 AA.
 AC Q9LAD6;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Mitogenic exotoxin z-9 (Fragment).
 GN SMEZ-9.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11299;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Mofitt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143659; AAF66659.1; -.
 DR HSSP: P13163; ISXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24213 MW; B21587BA343B5DD5 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 | | | | |
 Db 125 KTTVTAGEID 134

RESULT 8
 Q9LAD5 PRELIMINARY; PRT; 209 AA.
 AC Q9LAD5;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Mitogenic exotoxin z-10 (Fragment).
 GN SMEZ-10.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-11580;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Mofitt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL: AF143660; AAF66660.1; -.
 DR HSSP: P13163; ISXT.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24102 MW; 8B4C853751A56D06 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 | | | | |
 Db 125 KTTVTAGEID 134

RESULT 9
 Q9LAD4 PRELIMINARY; PRT; 209 AA.
 AC Q9LAD4;

DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=979;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143661; AAF66661.1; -.
DR HSP; P13163; ISXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B38D95DE CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 125 KTTVTAQOEID 134

RESULT 10
Q9LAD3 PRELIMINARY; PRT; 209 AA.
AC Q9LAD3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Mitogenic exotoxin Z-12 (Fragment).
GN SMEZ-12.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10303;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143662; AAF66662.1; -.
DR HSP; P13163; ISXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24086 MW; 1C4343235157DB68 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 125 KTTVTAQOEID 134

RESULT 11
Q9LAD2 PRELIMINARY; PRT; 209 AA.
AC Q9LAD2;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Mitogenic exotoxin Z-13 (Fragment).
GN SMEZ-13.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95/31;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143663; AAF66663.1; -.
DR HSP; P13163; ISXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24072 MW; 984C1B4614589A1E CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
DB 125 KTTVTAQOEID 134

RESULT 12
Q9LAD1 PRELIMINARY; PRT; 209 AA.
AC Q9LAD1;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Mitogenic exotoxin Z-14 (Fragment).
GN SMEZ-14.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4202;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143664; AAF66664.1; -.
DR HSP; P13163; ISXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.

DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 RT NON_TER 1
 SQ SEQUENCE 209 AA; 24122 MW; 0CF5D429E1B96EFE CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 | | | |
 Db 125 KTTVTAQED 134

RESULT 13
 O9LAD0 PRELIMINARY; PRT; 209 AA.

AC O9LAD0; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Mitogenic exotoxin z-15 (Fragment).
 GN SMEZ-15.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1314;
 [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-1;
 RX MEDLINE=20273982; PubMed=10811869;

RA Profit T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,

RT Fraser J.D.;
 RT Mosaic Structure, and Significant Antigenic Variation.*;

RL J. Exp. Med. 191:1765-1776(2000).

DR EMBL; AF143665; AAF6665.1; -.

DR HSSP; P13163; ISXT.

DR InterPro; IPR001961; Staph/Strep_toxin.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR Pfam; PF02876; Staph_Strep_tox_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER 1
 SQ SEQUENCE 209 AA; 24209 MW; B9097B4ABCD1474 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 | | | |
 Db 125 KTTVTAQED 134

RESULT 14
 O9LAC9 PRELIMINARY; PRT; 209 AA.

AC O9LAC9; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Mitogenic exotoxin z-16 (Fragment).
 GN SMEZ-16.

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1314;
 [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-10649;

RX MEDLINE=20273982; PubMed=10811869;

RA Profit T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,

RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.*";
 RL J. Exp. Med. 191:1765-1776(2000).

DR EMBL; AF143666; AAF6666.1; -.

DR HSSP; P13163; ISXT.

DR InterPro; IPR001961; Staph/Strep_toxin.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR Pfam; PF02876; Staph_Strep_tox_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER 1
 SQ SEQUENCE 209 AA; 24172 MW; A1DB8FA187098BA5 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 | | | |
 Db 125 KTTVTAQED 134

RESULT 15
 O9LAC8 PRELIMINARY; PRT; 209 AA.

AC O9LAC8; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Mitogenic exotoxin z-17 (Fragment).
 GN SMEZ-17.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1314;
 [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-11686;

RX MEDLINE=20273982; PubMed=10811869;

RA Profit T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,

RT Fraser J.D.;

RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.*";

RL J. Exp. Med. 191:1765-1776(2000).

DR EMBL; AF143667; AAF6667.1; -.

DR HSSP; P13163; ISXT.

DR InterPro; IPR001961; Staph/Strep_toxin.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR Pfam; PF02876; Staph_Strep_tox_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER 1
 SQ SEQUENCE 209 AA; 24181 MW; A33BF466398D9DC2 CRC64;

Query Match 72.7%; Score 24; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
 | | | |
 Db 125 KTTVTAQED 134

Search completed: June 5, 2003, 15:55:45
 Job time : 35.9091 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:47:43 ; Search time 40.7273 Seconds
(without alignments)
39.261 Million cell updates/sec

Title: US-09-150-947F-17
Perfect score: 28
Sequence: 1 XXXXXXXXXXXX 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	67.9	378	21	Arabidopsis thaliana
2	18	64.3	46	21	Gene 3 human secre
3	18	64.3	46	21	Human secreted pro
4	18	64.3	147	21	Human secreted pro
5	18	64.3	152	19	Rat ninjurin 1. R
6	18	64.3	152	19	Human ninjurin 1.
7	18	64.3	173	22	Novel human diagno
8	18	64.3	200	19	Human secreted pro
9	18	64.3	213	22	Plant D-like cycli
10	18	64.3	247	13	PCPD ORF 6. Chlam

11	18	64.3	284	23	ABP41256
12	18	64.3	406	17	AAW93144
13	18	64.3	420	17	AAW93155
14	18	64.3	420	17	AAW93157
15	18	64.3	618	22	ABG19070
16	18	64.3	705	17	AAW06831
17	18	64.3	765	22	AAW94373
18	18	64.3	765	22	AAW94373
19	18	64.3	768	21	AAW24448
20	17	60.7	17	23	ABW76254
21	17	60.7	17	23	ABW76259
22	17	60.7	24	21	AAW97855
23	17	60.7	24	21	AAW97862
24	17	60.7	24	22	AAW72193
25	17	60.7	24	22	AAW72200
26	17	60.7	75	23	ABP01309
27	17	60.7	76	22	ABG15641
28	17	60.7	88	22	AAO11663
29	17	60.7	99	21	AAW35163
30	17	60.7	100	21	AAW32693
31	17	60.7	106	21	AAW32693
32	17	60.7	142	19	AAW48373
33	17	60.7	142	20	AAW28249
34	17	60.7	142	21	AAW01389
35	17	60.7	142	22	AAW39026
36	17	60.7	143	22	ABW5735
37	17	60.7	143	22	ABW12218
38	17	60.7	150	20	AAW36961
39	17	60.7	153	21	AAW60296
40	17	60.7	170	23	ABW90300
41	17	60.7	171	21	AAW35162
42	17	60.7	184	22	ABW66316
43	17	60.7	186	21	AAW42925
44	17	60.7	188	21	AAW60286
45	17	60.7	189	21	AAW60295

ALIGNMENTS

RESULT 1	AAW35560	AAW35560 standard; Protein; 378 AA.
ID	AAW35560	
XX	AAW35560	
AC	AAW35560	
XX	AAW35560	
DT	18-OCT-2000	(first entry)
XX	AAW35560	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 43459.	
XX	AAW35560	
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
KW	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
XX	AAW35560	
PN	EP1033405-A2.	
XX	AAW35560	
PD	06-SEP-2000.	
XX	AAW35560	
PF	25-FEB-2000; 2000EP-0301439.	
XX	AAW35560	
PR	25-FEB-1999; 99US-0121825.	
PR	05-MAR-1999; 99US-0123180.	
PR	09-MAR-1999; 99US-0123548.	
PR	23-MAR-1999; 99US-0125788.	
PR	25-MAR-1999; 99US-0126264.	
PR	29-MAR-1999; 99US-0126785.	
PR	01-APR-1999; 99US-0127462.	
PR	06-APR-1999; 99US-0128234.	
PR	08-APR-1999; 99US-0128714.	
PR	16-APR-1999; 99US-0129845.	
PR	19-APR-1999; 99US-0130077.	

Human ovarian anti
S. lividans xylana
Streptomyces livid
Streptomyces livid
Novel human diagno
Major neutralising
Human APP-dependent
Human protein sequ
Human ORF22212
Staphylococcus aur
Staphylococcus aur
Staphylococcus aur
Staphylococcus aur
Peptide from regio
Human ORF22212
Novel human diagno
Human polypeptide
Zea mays protein f
Zea mays protein f
Human synthase-11k
Human ninjurin 2.
Human secreted pro
Human secreted pro
Human secreted pro
Human polypeptide
Human secreted pro
Protein involved 1
Arabidopsis thaliana
Human polypeptide
Zea mays protein f
Drosophila melanog
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana

PR 21-APR-1999;	99US-0130449.
PR 23-APR-1999;	99US-0130510.
PR 23-APR-1999;	99US-0130891.
PR 28-APR-1999;	99US-0131449.
PR 30-APR-1999;	99US-0132048.
PR 30-APR-1999;	99US-0132407.
PR 04-MAY-1999;	99US-0132484.
PR 05-MAY-1999;	99US-0132485.
PR 06-MAY-1999;	99US-0132486.
PR 07-MAY-1999;	99US-0132863.
PR 11-MAY-1999;	99US-0134256.
PR 14-MAY-1999;	99US-0134218.
PR 14-MAY-1999;	99US-0134219.
PR 14-MAY-1999;	99US-0134221.
PR 18-MAY-1999;	99US-0134370.
PR 19-MAY-1999;	99US-0134768.
PR 20-MAY-1999;	99US-0135124.
PR 21-MAY-1999;	99US-0135353.
PR 24-MAY-1999;	99US-0135629.
PR 25-MAY-1999;	99US-0136021.
PR 27-MAY-1999;	99US-0136392.
PR 28-MAY-1999;	99US-0136782.
PR 01-JUN-1999;	99US-0137222.
PR 03-JUN-1999;	99US-0137528.
PR 04-JUN-1999;	99US-0137502.
PR 07-JUN-1999;	99US-0137724.
PR 08-JUN-1999;	99US-0138094.
PR 10-JUN-1999;	99US-0138540.
PR 10-JUN-1999;	99US-0138847.
PR 14-JUN-1999;	99US-0139119.
PR 16-JUN-1999;	99US-0139453.
PR 16-JUN-1999;	99US-0139455.
PR 17-JUN-1999;	99US-0139492.
PR 18-JUN-1999;	99US-0139454.
PR 18-JUN-1999;	99US-0139455.
PR 18-JUN-1999;	99US-0139456.
PR 18-JUN-1999;	99US-0139457.
PR 18-JUN-1999;	99US-0139458.
PR 18-JUN-1999;	99US-0139459.
PR 18-JUN-1999;	99US-0139460.
PR 18-JUN-1999;	99US-0139461.
PR 18-JUN-1999;	99US-0139462.
PR 18-JUN-1999;	99US-0139463.
PR 18-JUN-1999;	99US-0139750.
PR 21-JUN-1999;	99US-0139763.
PR 22-JUN-1999;	99US-0139817.
PR 23-JUN-1999;	99US-0139899.
PR 23-JUN-1999;	99US-0140353.
PR 23-JUN-1999;	99US-0140354.
PR 24-JUN-1999;	99US-0140695.
PR 28-JUN-1999;	99US-0140823.
PR 29-JUN-1999;	99US-0140991.
PR 30-JUN-1999;	99US-0141287.
PR 01-JUL-1999;	99US-0141842.
PR 01-JUL-1999;	99US-0142153.
PR 02-JUL-1999;	99US-0142053.
PR 06-JUL-1999;	99US-0142390.
PR 08-JUL-1999;	99US-0142803.
PR 09-JUL-1999;	99US-0142920.
PR 12-JUL-1999;	99US-0142977.
PR 13-JUL-1999;	99US-0143542.
PR 14-JUL-1999;	99US-0143624.
PR 15-JUL-1999;	99US-0144005.
PR 16-JUL-1999;	99US-0144085.
PR 16-JUL-1999;	99US-0144086.
PR 19-JUL-1999;	99US-0144325.
PR 19-JUL-1999;	99US-0144331.
PR 19-JUL-1999;	99US-0144332.
PR 19-JUL-1999;	99US-0144333.
PR 19-JUL-1999;	99US-0144334.
PR 19-JUL-1999;	99US-0144335.
PR 20-JUL-1999;	99US-0144352.
PR 20-JUL-1999;	99US-0144632.
PR 21-JUL-1999;	99US-0144884.
PR 21-JUL-1999;	99US-0144814.
PR 21-JUL-1999;	99US-0145086.
PR 21-JUL-1999;	99US-0145088.
PR 22-JUL-1999;	99US-0145085.
PR 22-JUL-1999;	99US-0145087.
PR 22-JUL-1999;	99US-0145089.
PR 23-JUL-1999;	99US-0145192.
PR 23-JUL-1999;	99US-0145145.
PR 23-JUL-1999;	99US-0145218.
PR 23-JUL-1999;	99US-0145224.
PR 26-JUL-1999;	99US-0145276.
PR 27-JUL-1999;	99US-0145913.
PR 27-JUL-1999;	99US-0145918.
PR 27-JUL-1999;	99US-0145919.
PR 28-JUL-1999;	99US-0145951.
PR 02-AUG-1999;	99US-0146386.
PR 02-AUG-1999;	99US-0146388.
PR 02-AUG-1999;	99US-0146389.
PR 03-AUG-1999;	99US-0147038.
PR 04-AUG-1999;	99US-0147204.
PR 05-AUG-1999;	99US-0147302.
PR 05-AUG-1999;	99US-0147192.
PR 05-AUG-1999;	99US-0147260.
PR 06-AUG-1999;	99US-0147303.
PR 06-AUG-1999;	99US-0147416.
PR 09-AUG-1999;	99US-0147493.
PR 09-AUG-1999;	99US-0147935.
PR 10-AUG-1999;	99US-0148171.
PR 11-AUG-1999;	99US-0148319.
PR 12-AUG-1999;	99US-0148341.
PR 13-AUG-1999;	99US-0148565.
PR 16-AUG-1999;	99US-0148684.
PR 17-AUG-1999;	99US-0148368.
PR 18-AUG-1999;	99US-0148175.
PR 20-AUG-1999;	99US-0148426.
PR 20-AUG-1999;	99US-0148722.
PR 20-AUG-1999;	99US-0148723.
PR 20-AUG-1999;	99US-0148929.
PR 23-AUG-1999;	99US-0148902.
PR 23-AUG-1999;	99US-0148930.
PR 23-AUG-1999;	99US-0150566.
PR 26-AUG-1999;	99US-0150884.
PR 27-AUG-1999;	99US-0151065.
PR 27-AUG-1999;	99US-0151066.
PR 27-AUG-1999;	99US-0151080.
PR 30-AUG-1999;	99US-0151303.
PR 31-AUG-1999;	99US-0151338.
PR 01-SEP-1999;	99US-0151930.
PR 07-SEP-1999;	99US-0152363.
PR 10-SEP-1999;	99US-0153070.
PR 13-SEP-1999;	99US-0153758.
PR 15-SEP-1999;	99US-0154018.
PR 16-SEP-1999;	99US-0154039.
PR 20-SEP-1999;	99US-0154779.
PR 22-SEP-1999;	99US-0155139.
PR 23-SEP-1999;	99US-0155486.
PR 24-SEP-1999;	99US-0155659.
PR 28-SEP-1999;	99US-0156458.
PR 29-SEP-1999;	99US-0156596.
PR 04-OCT-1999;	99US-0157117.
PR 05-OCT-1999;	99US-0157753.
PR 06-OCT-1999;	99US-0157865.
PR 07-OCT-1999;	99US-0158029.
PR 08-OCT-1999;	99US-0158232.
PR 12-OCT-1999;	99US-0158369.
PR 13-OCT-1999;	99US-0159293.
PR 13-OCT-1999;	99US-0159294.
PR 13-OCT-1999;	99US-0159325.
PR 14-OCT-1999;	99US-0159329.
PR 14-OCT-1999;	99US-0159330.

PR 14-OCT-1999; 990S-0159331.
PR 14-OCT-1999; 990S-0159637.
PR 14-OCT-1999; 990S-0159638.
PR 18-OCT-1999; 990S-0159584.
PR 21-OCT-1999; 990S-0160741.
PR 21-OCT-1999; 990S-0160767.
PR 21-OCT-1999; 990S-0160770.
PR 21-OCT-1999; 990S-0160814.
PR 21-OCT-1999; 990S-0160815.
PR 22-OCT-1999; 990S-0160980.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161404.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 26-OCT-1999; 990S-0161359.
PR 26-OCT-1999; 990S-0161360.
PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161992.
PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

Query Match 67.9%; Score 19; DB 21; Length 378;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXKD 12
DB 13 KKAADAAALD 22

RESULT 2
AAB38172
ID AAB38172 standard; Protein; 46 AA.
AC AAB38172;
XX
DT 30-JAN-2001 (first entry)
DE Gene 3 human secreted protein homologous amino acid sequence #111.
XX
XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX
XX cerebroprotective; neoptropic; neuroprotective; antibacterial; virucide;
XX
XX fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
XX
XX hyperproliferative disorder; cardiovascular disorder; anglogenesis;
XX
XX cerebrovascular disorder; nervous system disorder; ocular disorder;
XX
XX wound healing; skin aging; food additive; preservative.

OS Homo sapiens.
XX
XX WO200058468-A2.
XX
XX PD 05-OCT-2000.
XX
XX PF 22-MAR-2000; 2000MO-US07526.
XX
XX PR 26-MAR-1999; 990S-0126600.
XX
XX PR 22-DEC-1999; 990S-0171550.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM, Komatsoulis G;
XX
XX DR WPI; 2000-611713/58.
XX
XX Nucleic acids encoding human secreted proteins, used to prevent, treat,
XX
XX PT ameliorate, or diagnose conditions such as autoimmune disorders, skin
XX
XX disorders and cancer -
XX
XX Dislosure; Page 362; 374pp; English.

XX
CC The polynucleotide sequences given in AAC69399 to AAC69445 encode the
CC
CC human secreted proteins given in AAB38119 to AAB38165. AAB38166 to
CC
CC AAB38201 represent human secreted polypeptide sequences and proteins
CC
CC homologous to them, which are given in the exemplification of the present
CC
CC invention. Human secreted proteins have activities based on the tissues
CC
CC and cells the genes are expressed in. Example of activities include:
CC
CC cytostatic; cardiant; vasotropic; cerebroprotective; neoptropic;
CC
CC neuroprotective; antibacterial; virucide; fungicide; and
CC
CC ophthalmological. The polynucleotides and polypeptides can be are used to
CC
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC
CC in diagnosing a pathological condition or susceptibility to a
CC
CC pathological condition. Disorders which are diagnosed or treated include
CC
CC autoimmune diseases, hyperproliferative disorders, cardiovascular
CC
CC disorders, cerebrovascular disorders, anglogenesis, nervous system
CC
CC disorders, infections caused by bacteria, viruses and fungi and ocular
CC
CC disorders. The polypeptides can also be used to aid wound healing and
CC
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC
CC maintain organs before transplantation, for supporting cell culture of
CC
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC
CC polypeptides can also be used as a food additive or preservative to
CC
CC increase or decrease storage capabilities. AAC69390 to AAC69398 and
CC
CC AAB38118 represent sequences used in the exemplification of the present
CC
CC invention.

SO Sequence 46 AA;
Query Match 64.3%; Score 18; DB 21; Length 46;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXKD 12
DB 19 KKSAAESMLD 28

RESULT 3
AAB38173
ID AAB38173 standard; Protein; 46 AA.
AC AAB38173;
XX
DT 30-JAN-2001 (first entry)
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:112.
XX
XX
XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX
XX cerebroprotective; neoptropic; neuroprotective; antibacterial; virucide;
XX
XX fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
XX
XX hyperproliferative disorder; cardiovascular disorder; anglogenesis;
XX
XX cerebrovascular disorder; nervous system disorder; ocular disorder;
XX
XX wound healing; skin aging; food additive; preservative.

OS Homo sapiens.
XX
XX WO200058468-A2.
XX
XX PD 05-OCT-2000.
XX
XX PF 22-MAR-2000; 2000MO-US07526.
XX
XX PR 26-MAR-1999; 990S-0126600.
XX
XX PR 22-DEC-1999; 990S-0171550.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM, Komatsoulis G;
XX
XX DR WPI; 2000-611713/58.

PT Nucleic acids encoding human secreted proteins, used to prevent, treat,
 PT ameliorate, or diagnose conditions such as autoimmune disorders, skin
 PT disorders and cancer -
 PS
 XX Disclosure; Page 362; 374pp; English.

CC The polynucleotide sequences given in AAC69399 to AAC69445 encode the
 CC human secreted proteins given in AAB38119 to AAB38165. AAB38166 to
 CC AAB38201 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Example of activities include:
 CC immunosuppressive; antiarthritic; antineumatic; antiproliferative;
 CC cytoprotective; cardiac; vasotropic; cerebroprotective; neurotropic;
 CC ophthalmological. The polynucleotides and polypeptides can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases, hyperproliferative disorders, cardiovascular
 CC disorders, cerebrovascular disorders, angiogenesis, nervous system
 CC disorders. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative and
 CC increase or decrease storage capabilities. AAC69399 to AAC69398 and
 CC AAB38118 represent sequences used in the exemplification of the present
 CC invention.

SQ Sequence 46 AA;

Query Match 64.3%; Score 18; DB 21; Length 46;

Best Local Similarity 40.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12

DB 19 KKSAAESWLD 28

RESULT 4

AAG02207 ID AAG02207 standard; Protein; 147 AA.

AC AAG02207;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 6288.

KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping.

OS Homo sapiens.

PN EPI033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GIST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR N-PSDB; AAC02213.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PS
 XX Claim 13; SEQ ID 6288; 71pp + CD-ROM; English.

CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.

SQ Sequence 147 AA;

Query Match 64.3%; Score 18; DB 21; Length 147;

Best Local Similarity 40.0%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12

DB 78 KKKRAATITLD 87

RESULT 5

AAW48271 ID AAW48271 standard; Protein; 152 AA.

AC AAW48271;

DT 23-JUN-1998 (first entry)

DE Rat ninjurin 1.

KM Rat; ninjurin; cellular adhesion molecule; membrane bound; tumour;

KW nerve injury induced gene; inflammation; nervous system.

OS Rattus sp.

PN WO9803650-A1.

PD 29-JAN-1998.

PF 24-JUL-1997; 97WO-US12210.

PR 24-JUL-1996; 96US-0672850.

PA (UNITW) UNITV WASHINGTON.

PI Araki T, MIdbrandt J;

DR WPI; 1998-120775/11.

DR N-PSDB; AAV20665.

PT New isolated nerve injury induced (ninjurin) gene - used to develop

PT products for treating conditions involving excessive or insufficient

PT cellular adhesion, e.g. inflammation or tumours

PS Claim 5; Fig 1B; 80pp; English.

CC The present sequence represents rat ninjurin 1 (nerve injury induced).
 CC The ninjurin protein (NP) plays a role in axonal regeneration of
 CC peripheral nervous system (PNS) neuronal cells after injury. The
 CC products can be used for developing products for treating ninjurin
 CC mediated disorders including conditions involving inappropriate (i.e.
 CC excessive or insufficient) cellular adhesion. Conditions involving

CC excessive cellular adhesion which may be treated include e.g.
 CC inflammatory diseases such as rheumatoid arthritis, asthma, allergy
 CC conditions, adult respiratory distress syndrome, inflammatory bowel
 CC diseases (e.g. Crohn's disease, ulcerative colitis and regional
 CC enteritis) and ophthalmic inflammatory diseases, autoimmune diseases,
 CC thrombosis or inappropriate platelet aggregation conditions,
 CC arteriosclerosis, reocclusion following thrombolysis, cardiovascular
 CC diseases, some forms of diabetes and neoplastic disease including
 CC metastasis conditions. The products can also be used to promote
 CC cellular adhesion, e.g. in nerve regeneration, wound healing or
 CC prosthetic implantation. The products can also be used for detection,
 CC purification, diagnosis and screening assays.

XX
 SQ Sequence 152 AA;

QY 3 KKKXXXXXLD 12
 II
 II
 DB 44 KKSAAESMLD 53

Query Match 64.3%; Score 18; DB 19; Length 152;
 Best Local Similarity 40.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 6
 AAW48272 standard; Protein; 152 AA.

XX AAW48272;
 XX
 DT 23-JUN-1998 (first entry)
 XX
 DE Human n1njurin 1.
 XX
 KM Human: n1njurin; cellular adhesion molecule; membrane bound; tumour;
 KW nerve injury induced gene; inflammation; nervous system.
 XX
 OS Homo sapiens.
 XX
 PN WC9803650-A1.
 XX
 PD 29-JAN-1998.
 XX
 PF 24-JUL-1997; 97WO-US12210.
 XX
 PR 24-JUL-1996; 96US-0672850.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Araki T, Milbrandt J;
 XX
 DR WPI; 1998-120775/11.
 DR N-PSDB; AAV20666.
 XX
 PT New isolated nerve injury induced (n1njurin) gene - used to develop
 PT products for treating conditions involving excessive or insufficient
 PT cellular adhesion, e.g. inflammation or tumours
 XX
 PS Claim 6; Fig 2B; 80pp; English.

CC The present sequence represents human n1njurin 1 (nerve injury induced).
 CC The n1njurin protein (NP) plays a role in axonal regeneration of
 CC peripheral nervous system (PNS) neuronal cells after injury. The
 CC products can be used for developing products for treating n1njurin
 CC mediated disorders including conditions involving inappropriate (i.e.
 CC excessive or insufficient) cellular adhesion. Conditions involving
 CC inflammatory diseases such as rheumatoid arthritis, asthma, allergy
 CC conditions, adult respiratory distress syndrome, inflammatory bowel
 CC diseases (e.g. Crohn's disease, ulcerative colitis and regional
 CC enteritis) and ophthalmic inflammatory diseases, autoimmune diseases,
 CC thrombosis or inappropriate platelet aggregation conditions,
 CC arteriosclerosis, reocclusion following thrombolysis, cardiovascular

CC diseases, some forms of diabetes and neoplastic disease including
 CC metastasis conditions. The products can also be used to promote
 CC cellular adhesion, e.g. in nerve regeneration, wound healing or
 CC prosthetic implantation. The products can also be used for detection,
 CC purification, diagnosis and screening assays.

XX
 SQ Sequence 152 AA;

QY 3 KKKXXXXXLD 12
 II
 II
 DB 44 KKSAAESMLD 53

Query Match 64.3%; Score 18; DB 19; Length 152;
 Best Local Similarity 40.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 7
 ABG20269 standard; Protein; 173 AA.

XX ABG20269;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #20260.
 XX
 KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEO INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS84456.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 50628; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 173 AA:

Query Match 64.3%; Score 18; DB 22; Length 173;
Best Local Similarity 40.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXXD 12
11
DB 141 KKAASHRALD 150

RESULT 8
AAMW74903
ID AAMW74903 standard; Protein; 200 AA.

XX AAMW74903;

DT 25-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 176 clone HFTBR48.

KW Human; secreted protein; testis; tumour; foetal brain tissue;
fusion protein; cancer; central nervous system; seizure;
diagnosis; neurodegenerative disease.

KX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 200 /label= unknown

PN WO9839448-A2.

PD 11-SEP-1998.

PF 06-MAR-1998; 98WO-US04493.

XX 02-OCT-1997; 97US-0061060.

PR 07-MAR-1997; 97US-0038621.

PR 07-MAR-1997; 97US-0040161.

PR 07-MAR-1997; 97US-0040162.

PR 07-MAR-1997; 97US-0040163.

PR 07-MAR-1997; 97US-0040333.

PR 07-MAR-1997; 97US-0040334.

PR 07-MAR-1997; 97US-0040336.

PR 07-MAR-1997; 97US-0040626.

PR 11-APR-1997; 97US-0043311.

PR 11-APR-1997; 97US-0043312.

PR 11-APR-1997; 97US-0043313.

PR 11-APR-1997; 97US-0043314.

PR 11-APR-1997; 97US-0043568.

PR 11-APR-1997; 97US-0043569.

PR 11-APR-1997; 97US-0043576.

PR 11-APR-1997; 97US-0043578.

PR 11-APR-1997; 97US-0043580.

PR 11-APR-1997; 97US-0043669.

PR 11-APR-1997; 97US-0043670.

PR 11-APR-1997; 97US-0043671.

PR 11-APR-1997; 97US-0043672.

PR 23-MAY-1997; 97US-0043674.

PR 23-MAY-1997; 97US-0044500.

PR 23-MAY-1997; 97US-0044501.

PR 23-MAY-1997; 97US-0044502.

PR 23-MAY-1997; 97US-004503.

PR 23-MAY-1997; 97US-004581.

PR 23-MAY-1997; 97US-004582.

PR 23-MAY-1997; 97US-004583.

PR 23-MAY-1997; 97US-004584.

PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056675.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Latleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;

PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 DR WPI: 1998-506364/43.
 DR N-PSDB: AAV59686.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 649-650; 721pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the nucleic
 CC acid molecule designated Gene 176 from the human cDNA clone HETBR48
 CC (deposited as clone ATCC 97904 and ATCC 209050).
 CC The gene can be used to generate fusion proteins by linking to the gene
 CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW4731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 CC
 SQ Sequence 200 AA;
 XX
 XX
 Query Match 64.3%; Score 18; DB 19; Length 200;
 Best Local Similarity 40.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 3 KKKXXXXXLD 12
 || ||
 DB 151 KKAASHRAID 160
 XX
 RESULT 9
 AAB47003
 ID AAB47003 standard; Protein; 213 AA.
 AC
 XX AAB47003;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Plant D-like cyclin inhibitor BRO2.
 XX
 KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
 KW growth rate; dividing cells; inactivation; protoplast; seed;
 KW root cell; meristem; leaf.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT Protein 20..147
 FT /label= BRO2
 XX
 PN MO200069883-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 15-MAY-2000; 2000MO-US13379.
 XX
 PR 14-MAY-1999; 99US-0134373.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 XX
 PI Roberts J, Kelly B;
 XX
 DR WPI: 2001-024998/03.
 DR N-PSDB: AAC85203.
 XX

PT Functionally inactivating expression of plant D-like cyclin inhibitor
 PT gene for producing a hyperplastic variant plant, modulating the growth
 PT and/or yield of plants, and increasing the proportion of dividing cells
 XX
 PS Example 1; Page 38-39; 50pp; English.
 XX
 CC The sequence given in AAB47003 represents a plant D1 cyclin
 CC inhibitor, BRO2. The DNA encoding this sequence was isolated using
 CC a yeast two hybrid screen. The BRO2 protein was found to contain a
 CC seven amino acid sequence cyclin binding domain similar to that of
 CC BRO1, BRO3 and BRO4 (See also AAB47005-6). The DNA encoding this
 CC sequence is homologous to a sequence present in a D-like cyclin
 CC inhibitor gene and when integrated at the corresponding locus,
 CC functionally inactivates plant D-like cyclin inhibitor protein
 CC expression. The BRO4 coding sequence may be used to produce a
 CC hyperplastic variant plant, increase the growth rate of a plant,
 CC or increase the proportion of dividing cells in a plant cell
 CC population, relative to a wild-type plant, by functionally
 CC inactivating the expression of a plant D-like cyclin inhibitor
 CC gene in a plant. BRO4 is useful for increasing the proportion of
 CC dividing cells in a plant cell population comprising protoplast,
 CC seeds, root cells, meristem cells or leaf cells.
 CC
 SQ Sequence 213 AA;
 XX
 XX
 Query Match 64.3%; Score 18; DB 22; Length 213;
 Best Local Similarity 40.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 3 KKKXXXXXLD 12
 || ||
 DB 10 KKKRTVTSID 19
 XX
 RESULT 10
 AAR29641
 ID AAR29641 standard; Protein; 247 AA.
 AC
 XX AAR29641;
 XX
 DT 05-FEB-1993 (first entry)
 XX
 DE PCTD ORF 6.
 XX
 KW CT; PCTD; epithelium; ocula mucosa; uro-genital mucosa; antigen;
 KW monoclonal; polyclonal; antibody; vaccine.
 XX
 OS Chlamydia trachomatis.
 XX
 PN EP499681-A.
 XX
 PD 26-AUG-1992.
 XX
 PF 17-APR-1991; 91EP-0106110.
 XX
 PR 07-FEB-1991; 91IT-0000314.
 XX
 PA (ISTS) SCLAVO SPA.
 XX
 PI Comanducci M, Giuliani MM, Ratti G, Tecce MF;
 XX
 DR WPI: 1992-285922/35.
 DR N-PSDB: AAQ27429.
 XX
 PT PCTD plasmid from Chlamydia Trachomatis and immunogenic proteins
 PT - for diagnosing and vaccinating against Chlamydia infections
 PT e.g. venereal lymphogranuloma
 XX
 PS Claim 1; Page 8-16; 40pp; English.
 XX
 CC The sequences given in AAR29636-43 are encoded by the plasmid isolated
 CC from Chlamydia trachomatis (CT) serotype D, PCTD. This serotype
 CC generally infects epithelial tissues, such as the ocular and

uro-genital mucous membranes, and shows a low virulence. Of the eight proteins encoded by the plasmid, seven are encoded by the sense strand and the eighth is encoded by the complementary strand. These proteins can be used as antigens for the preparation of poly- and mono-clonal antibodies to be used in diagnostics. The antigens can also be used in the formulation of vaccines against infections due to CT.

Sequence 247 AA:

Query Match 64.3%; Score 18; DB 13; Length 247;
Best Local Similarity 40.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
||
||
DB 13 KKNQTAASLD 22

RESULT 11

ABP41256
ID ABP41256 standard; Protein: 284 AA.

AC ABP41256;

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HOFNY16, SEQ ID NO:2388.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuroprotective;
antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

PN WO200200677-A1.

PD 03-JAN-2002.

PP 07-JUN-2001; 2001WO-US18569.

PR 07-JUN-2000; 2000US-209467P.

PA (HOMA-) HUMAN GENOME SCI INC.

PI Birse CE, Rosen CA;

DR WPI: 2002-147878/19.

DR N-PSDB; ABO54333.

Isolated nucleic acid molecules encoding novel ovarian polypeptides,
useful in the prevention, treatment and diagnosis of cancer (e.g.
neurological diseases -

Claim 11; SEQ ID NO 2388; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
ABP43228) and to cDNAs encoding them (ABO54131-ABO56305), and also
encompasses polypeptides 90% identical and polynucleotides 95% identical
to the sequences of the invention. The invention additionally relates to
recombinant vectors and host cells comprising human ovarian antigen
polynucleotides, antibodies against human ovarian antigens, and the use
of ovarian antigen polynucleotides and polypeptides in diagnosing,
treating, prognosing or preventing various ovarian and/or breast-related
disorders. Such conditions include ovarian cancer and breast cancer, and
metastatic tumours of ovarian or breast origin, reproductive system

disorders (e.g., infertility, disorders of pregnancy, anovulation,
polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
vaginitis), immune disorders (e.g., congenital and acquired
immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
blood-related disorders (e.g., anaemia), cardiovascular disorders,
respiratory disorders, neurological disorders, gastrointestinal disorders
and urinary system disorders. Ovarian antigen polypeptides and
polynucleotides may also be used in screening for compounds which
modulate ovarian antigen expression or activity. The polynucleotides may
further be used for gene therapy, chromosome mapping, in the
identification of individuals and in forensic analysis, and the
polypeptides may be used as food additives or to prepare antibodies
useful in disease diagnosis, drug targeting and phenotyping. The present
sequence represents a human ovarian antigen of the invention. The present
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 284 AA:

Query Match 64.3%; Score 18; DB 23; Length 284;
Best Local Similarity 40.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
||
||
DB 236 KKAASHRALD 245

RESULT 12

AAM93144
ID AAM93144 standard; Protein: 406 AA.

AC AAM93144;

DT 21-MAY-1999 (first entry)

DE S. lividans xylanase A protein StmXlnA.

Xylanase A; acidophilic; thermostable; XYL I; XYL II; plant biomass;
hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin.

OS Streptomyces lividans.

PN US5871730-A.

PD 16-FEB-1999.

PP 29-JUL-1994; 94US-0282197.

PR 29-JUL-1994; 94US-0282197.

PA (UYSH) UNIV SHERBROOKE.

PI Beaulieu C, Brzezinski R, Dery CV;

DR WPI: 1996-141348/15.

New acidophilic and thermostable xylanase enzymes from Actinomadura
sp. FC7 - useful for treating plant biomass, especially paper and
wood pulp, to degrade hemicellulose and hydrolyse xylan

Example 8; Fig 10; 60pp; English.

This invention describes the use of novel acidophilic and thermostable
xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
retain their activity under harsh industrial conditions (e.g. high
temperature or wide pH ranges) and may be secreted by recombinant host
cells, to treat plant biomass. Xylanases XYL I and XYL II are part of
a large group of hemicellulase enzymes and function by cutting the

CC beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose
CC residues that is a major constituent of hemicellulose). This means that
CC they may be used in the paper and pulp industry to improve the efficiency
CC of the bleaching process by degrading the structure of the material.
CC XYL I and XYL II may also be used to treat feed, by degrading a
CC substrate with a high beta-glucan or cellulose content. XYL I and XYL II
CC retain their activity at high temperatures (e.g. 70 deg. C) and at low
CC pHs (e.g. 4.0), conditions which tend to denature most known xylanases.
CC Enzymes that remain active in these conditions may be used in industrial
CC processes that are carried out at high temperature and low pH to speed up
CC other, non-enzymatic reactions, minimising costs, energy requirements,
CC and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
CC bleaching agents to penetrate better, to remove lignin from the pulp and
CC 'bleach' the colouration from it. This means smaller quantities of the
CC agents can be used to produce the same or a better result. Also,
CC disrupting the structure aids water drainage.
CC NOTE: This patent is an equivalent to FI9503640.

SQ Sequence 406 AA;

Query Match 64.3%; Score 18; DB 17; Length 406;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
|| ||
Db 330 KKAAYTAVLD 339

RESULT 13
AAW93155

ID AAW93155 standard; Protein; 420 AA.

XX AAW93155;

DT 21-MAY-1999 (first entry)

XX Streptomyces lividans xylanase A protein.

KW Xylanase A; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KW hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin.

XX Streptomyces lividans.

PN US5871730-A.

PD 16-FEB-1999.

PF 29-JUL-1994; 94US-0282197.

PR 29-JUL-1994; 94US-0282197.

XX (UYSH) UNIV SHERBROOKE.

PI Beaulieu C, Brzezinski R, Dery CV;

DR WPI; 1996-141348/15.

PT New acidophilic and thermostable xylanase enzymes from Actinomyadura
PT sp. FC7 - useful for treating plant biomass, especially paper and
PT wood pulp, to degrade hemicellulose and hydrolyse xylan

XX Example 8; Fig 11; 60pp; English.

CC This invention describes the use of novel acidophilic and thermostable
CC xylanase enzymes (XYL I and XYL II) from Actinomyadura sp. FC7 which
CC retain their activity under harsh industrial conditions (e.g. high
CC temperature or wide pH ranges) and may be secreted by recombinant host
CC cells, to treat plant biomass. Xylanases XYL I and XYL II are part of
CC a large group of hemicellulase enzymes and function by cutting the

CC beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose
CC residues that is a major constituent of hemicellulose). This means that
CC they may be used in the paper and pulp industry to improve the efficiency
CC of the bleaching process by degrading the structure of the material.
CC XYL I and XYL II may also be used to treat feed, by degrading a
CC substrate with a high beta-glucan or cellulose content. XYL I and XYL II
CC retain their activity at high temperatures (e.g. 70 deg. C) and at low
CC pHs (e.g. 4.0), conditions which tend to denature most known xylanases.
CC Enzymes that remain active in these conditions may be used in industrial
CC processes that are carried out at high temperature and low pH to speed up
CC other, non-enzymatic reactions, minimising costs, energy requirements,
CC and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
CC bleaching agents to penetrate better, to remove lignin from the pulp and
CC 'bleach' the colouration from it. This means smaller quantities of the
CC agents can be used to produce the same or a better result. Also,
CC disrupting the structure aids water drainage.
CC NOTE: This patent is an equivalent to FI9503640.

SQ Sequence 420 AA;

Query Match 64.3%; Score 18; DB 17; Length 420;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
|| ||
Db 330 KKAAYTAVLD 339

RESULT 14
AAW93157

ID AAW93157 standard; Protein; 420 AA.

XX AAW93157;

DT 21-MAY-1999 (first entry)

XX Streptomyces lividans xylanase A protein.

KW Xylanase A; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KW hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin.

XX Streptomyces lividans.

PN US5871730-A.

PD 16-FEB-1999.

PF 29-JUL-1994; 94US-0282197.

PR 29-JUL-1994; 94US-0282197.

XX (UYSH) UNIV SHERBROOKE.

PI Beaulieu C, Brzezinski R, Dery CV;

DR WPI; 1996-141348/15.

PT New acidophilic and thermostable xylanase enzymes from Actinomyadura
PT sp. FC7 - useful for treating plant biomass, especially paper and
PT wood pulp, to degrade hemicellulose and hydrolyse xylan

XX Example 9; Fig 13; 60pp; English.

CC This invention describes the use of novel acidophilic and thermostable
CC xylanase enzymes (XYL I and XYL II) from Actinomyadura sp. FC7 which
CC retain their activity under harsh industrial conditions (e.g. high
CC temperature or wide pH ranges) and may be secreted by recombinant host
CC cells, to treat plant biomass. Xylanases XYL I and XYL II are part of
CC a large group of hemicellulase enzymes and function by cutting the

CC beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose
 CC residues that is a major constituent of hemicellulose). This means that
 CC they may be used in the paper and pulp industry to improve the efficiency
 CC of the bleaching process by degrading the structure of the material.
 CC XYL I and XYL II may also be used to treat feed, by degrading a
 CC substrate with a high beta-glucan or cellulose content. XYL I and XYL II
 CC retain their activity at high temperatures (e.g. 70 deg. C) and at low
 CC pHs (e.g. 4.0), conditions which tend to denature most known xylanases.
 CC Enzymes that remain active in these conditions may be used in industrial
 CC processes that are carried out at high temperature and low pH to speed up
 CC other, non-enzymatic reactions, minimising costs, energy requirements,
 CC and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
 CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
 CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
 CC bleaching agents to penetrate better, to remove lignin from the pulp and
 CC 'bleach' the colouration from it. This means smaller quantities of the
 CC agents can be used to produce the same or a better result. Also,
 CC disrupting the structure aids water drainage.
 CC NOTE: This patent is an equivalent to F19503640.

XX SQ Sequence 420 AA;

Query Match Best Local Similarity 64.3%; Score 18; DB 17; Length 420;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXXLD 12
 || ||
 DB 330 KKAATYAVLD 339

RESULT 15

ABG19070 ID ABG19070 standard; Protein; 618 AA.

AC ABG19070;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #19061.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS83357.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity

XX Claim 20; SEQ ID No 49429; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG0377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 618 AA;

Query Match Best Local Similarity 64.3%; Score 18; DB 22; Length 618;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXXLD 12
 || ||
 DB 372 KKVTLSTSLD 381

Search completed: June 5, 2003, 16:00:25
 Job time : 40.7273 secs

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OM protein - protein search, using sw model

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Title: US-09-150-947f-17
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	64.3	100	4	US-08-672-850-13
2	18	64.3	152	4	US-08-672-850-4
3	18	64.3	152	4	US-08-672-850-6
4	18	64.3	152	4	US-08-672-850-12
5	18	64.3	200	4	US-09-149-476-495
6	18	64.3	237	2	US-08-933-750C-32
7	18	64.3	237	2	US-09-234-613-32
8	18	64.3	247	3	US-08-969-644-18
9	18	64.3	247	3	US-08-444-189-18
10	18	64.3	247	3	US-08-468-544-18
11	18	64.3	406	2	US-08-282-197C-52
12	18	64.3	420	2	US-08-282-197C-63
13	18	64.3	420	2	US-08-282-197C-66
14	18	64.3	451	2	US-08-468-812-8
15	18	64.3	451	2	US-08-590-563-8
16	18	64.3	705	2	US-08-663-566A-19
17	18	64.3	705	2	US-08-023-610-19
18	18	64.3	705	2	US-08-288-065A-19
19	18	64.3	705	2	US-08-362-240A-19
20	18	64.3	705	5	PCP-US95-10245-19
21	18	64.3	705	5	US-08-996-933-6
22	17	60.7	17	4	US-08-896-933-19
23	17	60.7	17	4	US-09-314-235-6
24	17	60.7	17	4	US-09-314-235-19
25	17	60.7	24	3	US-08-838-413A-20
26	17	60.7	24	3	US-08-838-413A-27
27	17	60.7	142	4	US-08-672-850-8

28	17	60.7	193	4	US-08-896-933-31	Sequence 31, Appl
29	17	60.7	193	4	US-09-314-235-31	Sequence 31, Appl
30	17	60.7	194	1	US-08-446-918A-6	Sequence 6, Appl
31	17	60.7	194	2	US-08-580-806-6	Sequence 6, Appl
32	17	60.7	234	1	US-08-152-456A-2	Sequence 2, Appl
33	17	60.7	234	1	US-08-440-221-2	Sequence 2, Appl
34	17	60.7	234	3	US-08-486-099-111	Sequence 11, App
35	17	60.7	234	3	US-08-360-107A-121	Sequence 121, App
36	17	60.7	234	3	US-08-484-223B-111	Sequence 111, App
37	17	60.7	234	3	US-08-919-597-111	Sequence 111, App
38	17	60.7	234	3	US-08-475-668A-111	Sequence 111, App
39	17	60.7	234	3	US-08-485-551A-111	Sequence 111, App
40	17	60.7	234	3	US-08-471-913A-111	Sequence 111, App
41	17	60.7	234	4	US-08-485-264A-111	Sequence 111, App
42	17	60.7	234	4	US-08-474-239A-111	Sequence 111, App
43	17	60.7	238	4	US-09-144-776B-12	Sequence 12, Appl
44	17	60.7	238	4	US-08-896-933-28	Sequence 28, Appl
45	17	60.7	238	4	US-09-314-235-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-672-850-13
; Sequence 13, Application US/08672850
; Patent No. 6140117
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey
APPLICANT: Ataki, Toshiyuki
TITLE OF INVENTION: NINURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672, 850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-672-850-13

Query Match 64.3%; Score 18; DB 4; Length 100;
Best Local Similarity 40.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 XXXXXXXXXXLD 12
DB 44 KKSNAESMLD 53

```
RESULT 2
US-08-672-850-4
; Sequence 4, Application US/08672850
; Patent No. 6140117
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey
; APPLICANT: Arai, Toshiyuki
; TITLE OF INVENTION: NINTURIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,850
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-63610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-672-850-4

Query Match          64.3%; Score 18; DB 4; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
DB 44 KKSAAESMLD 53

RESULT 3
US-08-672-850-6
; Sequence 6, Application US/08672850
; Patent No. 6140117
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey
; APPLICANT: Arai, Toshiyuki
; TITLE OF INVENTION: NINTURIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,850
```

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; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-63610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-672-850-6

Query Match          64.3%; Score 18; DB 4; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
DB 44 KKSAAESMLD 53

RESULT 4
US-08-672-850-12
; Sequence 12, Application US/08672850
; Patent No. 6140117
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey
; APPLICANT: Arai, Toshiyuki
; TITLE OF INVENTION: NINTURIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,850
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-63610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-672-850-12

Query Match          64.3%; Score 18; DB 4; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
```

Db 44 KKSASMSLD 53

RESULT 5
US-09-149-476-495

Sequence 495, Application US/09149476
Patent No. 6420526

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002PI

CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,601

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892

EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 64.3%; Score 18; DB 4; Length 200;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXD 12
11
Db 151 KKAASHRAD 160

RESULT 6
US-08-933-750C-32
; Sequence 32, Application US/08933750C

Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1602473
US-08-933-750C-32

Query Match 64.3%; Score 18; DB 2; Length 237;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXD 12
11
Db 189 KKAASHRAD 198

RESULT 7
US-09-234-613-32
; Sequence 32, Application US/09234613
; Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1602473
US-09-234-613-32

Query Match 64.3%; Score 18; DB 4; Length 237;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXD 12
DB 189 KKAASHRALD 198

RESULT 8
US-08-969-644-18
Sequence 18, Application US/08969644
Patent No. 6096519
GENERAL INFORMATION:
APPLICANT: Rattl, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM, RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-969-644-18

Query Match 64.3%; Score 18; DB 3; Length 247;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXD 12
DB 13 KKNQTAASLD 22

RESULT 9
US-08-444-189-18
Sequence 18, Application US/08444189
Patent No. 6110705
GENERAL INFORMATION:
APPLICANT: Rattl, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM, RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820

FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-189-18

Query Match 64.3%; Score 18; DB 3; Length 247;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
DB 13 KKNQTAASLD 22

RESULT 10
US-08-468-544-18
Sequence 18, Application US/08468544
Patent No. 6248363

GENERAL INFORMATION:
APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Gulianl, Marzia M.
TITLE OF INVENTION: PC12 PLASID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-544-18

Query Match 64.3%; Score 18; DB 4; Length 247;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
DB 13 KKNQTAASLD 22

RESULT 11
US-08-282-197C-52
Sequence 52, Application US/08282197C
Patent No. 5871730

GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V.
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-52

Query Match

Best Local Similarity 64.3%; Score 18; DB 2; Length 406;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
DB 330 KKAAYTAVLD 339

RESULT 12

US-08-282-197C-63
Sequence 63, Application US/08282197C
Patent No. 5871730

GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V.
APPLICANT: Beaulieu, Carole

TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-63

Query Match 64.3%; Score 18; DB 2; Length 420;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXD 12
DB 330 KKAAYTAVLD 339

RESULT 13
US-08-282-197C-66
Sequence 66, Application US/08282197C
Patent No. 5871730
GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-66

Query Match 64.3%; Score 18; DB 2; Length 420;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXD 12
DB 330 KKAAYTAVLD 339

RESULT 14
US-08-468-812-8
Sequence 8, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaenper, Jari
APPLICANT: M ntyl, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tinja
APPLICANT: Kisto, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-468-812-8

Query Match
Best Local Similarity 64.3%; Score 18; DB 2; Length 491;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXD 12
DB 333 KKAAYTAVLD 342

Query Match
Best Local Similarity 64.3%; Score 18; DB 4; Length 491;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 KXXXXXXD 12
DB 333 KKAAYTAVLD 342
Search completed: June 5, 2003, 15:32:44
Job time : 10.5455 secs

RESULT 15

US-08-590-563-8
Sequence 8, Application US/08590563

Patent No. 6300114

GENERAL INFORMATION:

APPLICANT: M nely, Arja
APPLICANT: Vehmaaper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Jari
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-590-563-8

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:01 ; Search time 14.5455 Seconds
(without alignments)
85.173 Million cell updates/sec

Title: US-09-150-947f-17
Perfect score: 28
Sequence: 1 XXXXXXXXXXXXLD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	64.3	200	9	US-09-809-391-495 Sequence 495, App
2	18	64.3	237	10	US-09-840-787-32 Sequence 32, App1
3	18	64.3	365	9	US-10-125-692-16 Sequence 16, App1
4	18	64.3	491	10	US-09-770-621-8 Sequence 8, App1
5	17	60.7	12	9	US-10-113-809-3 Sequence 3, App1
6	17	60.7	58	12	US-10-001-879-145 Sequence 145, App
7	17	60.7	107	9	US-09-465-714-4 Sequence 4, App1
8	17	60.7	142	10	US-09-729-674-76 Sequence 76, App1
9	17	60.7	151	9	US-09-465-714-2 Sequence 2, App1
10	17	60.7	194	9	US-09-465-714-3 Sequence 3, App1
11	17	60.7	233	1	US-08-882-431-12 Sequence 12, App1
12	17	60.7	234	9	US-09-870-759-18 Sequence 18, App1
13	17	60.7	234	9	US-10-002-784-12 Sequence 12, App1
14	17	60.7	238	9	US-09-465-714-1 Sequence 1, App1
15	17	60.7	266	1	US-08-882-431-14 Sequence 14, App1
16	17	60.7	266	9	US-09-870-759-12 Sequence 12, App1
17	17	60.7	266	9	US-10-002-784A-14 Sequence 14, App1
18	17	60.7	383	9	US-09-738-626-6821 Sequence 6821, App
19	17	60.7	490	10	US-09-841-132-434 Sequence 434, App

20	17	60.7	582	9	US-10-046-938-29 Sequence 29, App1
21	17	60.7	623	9	US-09-738-626-5990 Sequence 5990, App
22	16	57.1	10	10	US-09-150-947B-3 Sequence 3, App1
23	16	57.1	10	10	US-09-150-947B-4 Sequence 4, App1
24	16	57.1	12	9	US-10-113-809-1 Sequence 1, App1
25	16	57.1	12	9	US-10-113-809-4 Sequence 4, App1
26	16	57.1	12	10	US-09-150-947B-2 Sequence 2, App1
27	16	57.1	13	10	US-09-150-947B-5 Sequence 5, App1
28	16	57.1	13	10	US-09-150-947B-6 Sequence 6, App1
29	16	57.1	13	10	US-09-150-947B-11 Sequence 11, App1
30	16	57.1	14	10	US-09-150-947B-9 Sequence 9, App1
31	16	57.1	14	10	US-09-150-947B-10 Sequence 10, App1
32	16	57.1	16	10	US-09-150-947B-7 Sequence 7, App1
33	16	57.1	25	10	US-09-803-165-29 Sequence 29, App1
34	16	57.1	26	10	US-09-150-947B-1 Sequence 1, App1
35	16	57.1	35	10	US-09-150-947B-8 Sequence 8, App1
36	16	57.1	36	9	US-09-764-891-4313 Sequence 4313, App
37	16	57.1	38	10	US-09-071-838-150 Sequence 150, App
38	16	57.1	39	10	US-09-843-845-12 Sequence 12, App1
39	16	57.1	63	9	US-10-044-692-65 Sequence 65, App1
40	16	57.1	63	9	US-10-044-539-65 Sequence 65, App1
41	16	57.1	69	9	US-09-843-676-16 Sequence 16, App1
42	16	57.1	69	9	US-09-766-253-16 Sequence 16, App1
43	16	57.1	69	9	US-09-438-486-16 Sequence 16, App1
44	16	57.1	69	9	US-10-053-758-16 Sequence 16, App1
45	16	57.1	69	9	US-10-054-295-16 Sequence 16, App1

ALIGNMENTS

RESULT 1
US-09-809-391-495
Sequence 495, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 495
LENGTH: 200
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (200)
OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-495

Query Match 64.3% Score 18; DB 9; Length 200;
Best Local Similarity 40.0% Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXXXXLD 12
DB 151 KKAASHRALD 160

RESULT 2
US-09-840-787-32
Sequence 32, Application US/09840787
Patent No. US20020058264A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice

Yue, Henry
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1602473
SEQUENCE DESCRIPTION: SEQ ID NO: 32 :
US-09-840-787-32
Query Match 64.3% Score 18; DB 10; Length 237;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 KKKXXXXLTD 12
DB 189 KKAASHRALD 198
RESULT 3
US-10-125-692-16
Sequence 16, Application US/10125692
Publication No. US20030044429a1
GENERAL INFORMATION:
APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka
APPLICANT: Smith, Kelly D.
APPLICANT: Underhill, David M.
APPLICANT: Ozlinsky, Adrian
TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
TITLE OF INVENTION: of use
FILE REFERENCE: P-1S 5155
CURRENT APPLICATION NUMBER: US/10/125,692
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16

LENGTH: 365
TYPE: PRT
ORGANISM: P. mirabilis1
US-10-125-692-16
Query Match 64.3% Score 18; DB 9; Length 365;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 KKKXXXXLTD 12
DB 197 KKNMAATLTD 206
RESULT 4
US-09-770-621-8
Sequence 8, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M ntyl, Arja
APPLICANT: Vehmaaper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Paloneimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-09-770-621-8

Query Match 64.3%; Score 18; DB 10; Length 491;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXD 12
DB 333 KKAAYTAVLD 342

RESULT 5

US-10-113-809-3
Sequence 3, Application US/10113809
Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Maschke, Hans, E.
TITLE OF INVENTION: EXOTOXIN-LIGAND
FILE REFERENCE: MBP-011XX
CURRENT APPLICATION NUMBER: US/10/113,809
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 101 16 042.9-41
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacterial Toxin Binding Ligand
US-10-113-809-3

Query Match 60.7%; Score 17; DB 9; Length 12;
Best Local Similarity 40.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXD 12
DB 3 KKOALAISTLD 12

RESULT 6

US-10-001-879-145
Sequence 145, Application US/10001879
Patent No. US20020127237A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Reclon, Hervé
APPLICANT: Caferkey, Robert
APPLICANT: Ali, Shujath
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0281
CURRENT APPLICATION NUMBER: US/10/001,879
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,188
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PatentIn version 3.1
SEQ ID NO 145
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-879-145

Query Match 60.7%; Score 17; DB 12; Length 58;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXD 12
DB 11

DB 42 KKKRTQATLD 51

RESULT 7

US-09-465-714-4
Sequence 4, Application US/09465714
Publication No. US20030032582A1
GENERAL INFORMATION:
APPLICANT: Wahlsten, Jennifer L.
APPLICANT: Ramakrishnan, S.
APPLICANT: Schlievert, Patrick M.
TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
FILE REFERENCE: 09531/003001
CURRENT APPLICATION NUMBER: US/09/465,714
CURRENT FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: 09/001,593
PRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Truncated bacterial sequence
US-09-465-714-4

Query Match 60.7%; Score 17; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXD 12
DB 34 KKOALAISTLD 43

RESULT 8

US-09-729-674-76
Sequence 76, Application US/09729674
Patent No. US20010039335A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavaille, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steindinger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Recheil, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 76
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
US-09-729-674-76

Query Match 60.7%; Score 17; DB 10; Length 142;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 30 KKSVAESMLD 39

RESULT 9

US-09-465-714-2
; Sequence 2, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid containing bacterial and mammalian sequence
US-09-465-714-2

Query Match 60.7%; Score 17; DB 9; Length 151;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 34 KKOALAISTLD 43

RESULT 10

US-09-465-714-3
; Sequence 3, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Bacterial Sequence
US-09-465-714-3

Query Match 60.7%; Score 17; DB 9; Length 194;
Best Local Similarity 40.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 121 KKOALAISTLD 130

RESULT 11
US-08-882-431-12
; Sequence 12, Application US/08882431
; Publication No. US20030009015A1

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: John Moran
STREET: US Army MCMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DERRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Moran, John
REGISTRATION NUMBER: 26,313

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEFAX: (301) 619-7714
TELEPHONE: (301) 619-2065

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

LENGTH: 233
TYPE: Amino Acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide
US-08-882-431-12

Query Match 60.7%; Score 17; DB 1; Length 233;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 160 KKOALAISTLD 169

RESULT 12

US-09-870-759-18
; Sequence 18, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-18

Query Match 60.7%; Score 17; DB 9; Length 234;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
11
11

Db 161 KKOLAISTLD 170

RESULT 13
US-10-002-784A-12
; Sequence 12, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: toxin shock syndrom toxin-1 mutant
US-10-002-784A-12

Query Match 60.7%; Score 17; DB 9; Length 234;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
11
11

Db 161 KKOLAISTLD 170

RESULT 14
US-09-465-714-1
; Sequence 1, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid containing bacterial and mammalian sequence
US-09-465-714-1

Query Match 60.7%; Score 17; DB 9; Length 238;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
11
11

Db 121 KKOLAISTLD 130

RESULT 15

US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-2065
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-14

Query Match 60.7%; Score 17; DB 1; Length 266;
Best Local Similarity 40.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12
11
11

Db 178 KKSVTAEID 187

Search completed: June 5, 2003, 15:49:05
Job time: 14.5455 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:24:01 ; Search time 11.8162 Seconds
(without alignments)
97.613 Million cell updates/sec

Title: US-09-150-947f-17
Perfect score: 28
Sequence: 1 XXXXXXXXXXXX 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	67.9	284	2	conserved hypothet
2	19	67.9	378	2	probable elongatio
3	18	64.3	100	1	ribosomal protein
4	18	64.3	159	2	hypothetical prote
5	18	64.3	161	2	transcription regu
6	18	64.3	169	2	hypothetical prote
7	18	64.3	171	2	hypothetical prote
8	18	64.3	212	2	probable tet opero
9	18	64.3	212	2	probable tet opero
10	18	64.3	212	2	probable tet opero
11	18	64.3	217	2	probable transcript
12	18	64.3	237	2	hypothetical prote
13	18	64.3	247	2	hypothetical prote
14	18	64.3	247	2	hypothetical prote
15	18	64.3	278	2	hypothetical prote
16	18	64.3	278	2	hypothetical prote
17	18	64.3	344	2	hypothetical prote
18	18	64.3	344	2	hypothetical prote
19	18	64.3	365	2	probable portal pr
20	18	64.3	383	2	flagellin flhC-1 -
21	18	64.3	413	2	MG349 homolog G12
22	18	64.3	427	2	actin like protein
23	18	64.3	477	1	endo-1,4-beta-xyla
24	18	64.3	533	2	hypothetical prote
25	18	64.3	837	2	hypothetical prote
26	18	64.3	858	2	hypothetical prote
27	18	64.3	863	2	probable permease,
28	18	64.3	1035	2	hypothetical prote
29	18	64.3	1279	2	hypothetical prote
					protoporphylin IX

30	17	60.7	109	2	A69448	hypothetical prote
31	17	60.7	118	2	T15655	hypothetical prote
32	17	60.7	137	2	G71541	probable camp-depe
33	17	60.7	137	2	C81695	cyclic nucleotide-
34	17	60.7	156	2	S23357	H+-transporting tw
35	17	60.7	185	2	G64084	3-methyladenine DN
36	17	60.7	186	2	S66070	conserved hypothet
37	17	60.7	207	2	AC2950	transcription regu
38	17	60.7	213	2	H98332	probable transcript
39	17	60.7	217	1	B64222	heat shock protein
40	17	60.7	223	2	H84977	ribose-5-phosphate
41	17	60.7	226	2	A86268	hypothetical prote
42	17	60.7	234	1	XCSAS1	toxic shock syndro
43	17	60.7	234	2	B89992	toxic shock syndro
44	17	60.7	234	2	C69519	conserved hypothet
45	17	60.7	239	2	A83953	uridylylate kinase s

ALIGNMENTS

RESULT 1
T50261
conserved hypothetical protein SPAC890.05 with G-patch domain [imported] - fission ye
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50261
R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
A:Reference number: Z25052
A:Accession: T50261
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-284 <SAND>
A:Cross-references: EMBL:AL133498; PIDN:CA863496.1; GSPDB:GN00066; SPDB:SPAC890.05
A:Experimental source: strain 972n(-); cosmid c890
C:Genetics:
A:Gene: SPDB:SPAC890.05
A:Map position: 1

Query Match 67.9% Score 19; DB 2; Length 284;
Best Local Similarity 40.0%; Pred. No. 6.8;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXLD 12
DB 179 KKTGTGSLD 188

RESULT 2
E84806
probable elongation factor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84806
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Crokin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402:761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84806
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <STO>
A:Cross-references: GB:AE002093; MID:93786016; PIDN:AAC67362.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g38560
A:Map position: 2

Query Match 67.9% Score 19; DB 2; Length 378;
Best Local Similarity 40.0%; Pred. No. 8.8;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXL 12
 ||
 DB 13 KKAADAAALD 22

RESULT 3

RVLV14
 C:Species: chloroplast protein S14, chloroplast - liverwort (Marchantia polymorpha) chloroplast
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999
 C:Accession: A02733; S01876

R:Ohnaka, K.
 submitted to the EMBL Data Library, October 1986

A:Reference number: A00150
 A:Accession: A02733

A:Molecule type: DNA
 A:Residues: 1-100 <OH>

R:Ohnaka, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
 Nature 322, 572-574, 1986

A:Title: Chloroplast gene organization deduced from complete sequence of liverwort March
 A:Reference number: A38014

A:Contents: annotation; gene organization, sites, features

R:Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T
 J. Mol. Biol. 203, 299-331, 1988

A:Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gen
 A:Reference number: S01567; MUID:89068686; PMID:2974085

A:Accession: S01876
 A:Molecule type: DNA

A:Residues: 1-100 <UME>
 A:Cross-references: GB:X04465; GB:Y00686; NID:g11640; PIDN:CAA28083.1; PID:g11670

C:Genetics:

A:Gene: rps14
 A:Genome: chloroplast

C:Superfamily: Escherichia coli ribosomal protein S14
 C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 64.3%; Score 18; DB 1; Length 100;
 Best Local Similarity 40.0%; Pred. No. 7.8;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXL 12
 ||
 DB 29 KKTETSSLD 38

RESULT 4

T48837
 hypothetical protein 68B2.210 [imported] - Neurospora crassa

C:Species: Neurospora crassa
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001

C:Accession: T48837
 R:Schulte, U.; Altmann, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24541
 A:Accession: T48837

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-159 <SCH>

A:Cross-references: EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.210

A:Experimental source: cosmid contig 68B2; strain 74

C:Genetics:

A:Gene: NCSP:68B2.210
 A:Map position: 2

C:Superfamily: Neurospora crassa hypothetical protein 68B2.210

Query Match 64.3%; Score 18; DB 2; Length 159;
 Best Local Similarity 40.0%; Pred. No. 12;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXL 12
 ||
 DB 71 KKTALASLD 80

RESULT 5
 AB2401
 transcription regulator Ycr family VCA0917 [imported] - Vibrio cholerae (strain N169

C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: AB2401

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drygol, I.; Sellers

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: AB2401

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-161 <HEI>

A:Cross-references: GB:AE004420; GB:AE003853; NID:g9658361; PIDN:AAF96814.1; GSPDB:GN

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VCA0917
 A:Map position: 2

Query Match 64.3%; Score 18; DB 2; Length 161;
 Best Local Similarity 40.0%; Pred. No. 12;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXL 12
 ||
 DB 62 KKTDFASALD 71

RESULT 6

S07748
 hypothetical protein 13 - Paramecium tetraurelia mitochondrion

C:Species: mitochondrion Paramecium tetraurelia
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-Dec-1999

C:Accession: S07748

R:Pritchard, A.E.; Seilhammer, J.J.; Mahalingam, R.; Sable, C.L.; Venutti, S.E.; Cummin
 Nucleic Acids Res. 18, 173-180, 1990

A:Title: Nucleotide sequence of the mitochondrial genome of Paramecium.

A:Reference number: S07745; MUID:90174913; PMID:2308823

A:Accession: S07748

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-169 <PRI>

A:Cross-references: EMBL:X15917; NID:g13256; PID:g578763

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

A:Start codon: ATA

C:Superfamily: Paramecium tetraurelia mitochondrion hypothetical protein 13

Query Match 64.3%; Score 18; DB 2; Length 169;
 Best Local Similarity 40.0%; Pred. No. 13;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXL 12
 ||
 DB 36 KKTSTYSKLD 45

RESULT 7

A96723
 hypothetical protein F20P5.23 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96723

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani, R.; Moore, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A96723

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <STO>

A:Cross-references: GB:AE005173; NID:g2194134; PIDN:AAB61109.1; GSPDB:GN00141

C:Genetics:

A:Gene: F20P5.23

A:Map position: 1

Query Match

Best Local Similarity 64.3%; Score 18; DB 2; Length 171;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12

DB 16 KKLTTDALD 25

RESULT 8

C90786

probable tet operon regulator [imported] - *Escherichia coli* (strain O157:H7, substrain F)

C:Species: *Escherichia coli*

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: C90786

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Ref. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genome

A:Reference number: A9629; MUID:21156231; PMID:11258796

A:Accession: C90786

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <NAV>

A:Cross-references: GB:BA000007; PIDN:BA834682.1; PID:g13360719; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: ECS1259

Query Match

Best Local Similarity 64.3%; Score 18; DB 2; Length 212;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12

DB 20 KKAIISSALD 29

RESULT 9

A85646

probable tet operon regulator ycdC [imported] - *Escherichia coli* (strain O157:H7, substrain F)

C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A85646

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85646

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <STO>

A:Cross-references: GB:AE005174; NID:g12514373; PIDN:AAG55629.1; GSPDB:GN00145; OMGP:Z15

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: ycdC

Query Match

Best Local Similarity 64.3%; Score 18; DB 2; Length 212;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12

DB 20 KKAIISSALD 29

RESULT 10

C64843

probable transcription regulator ycdC - *Escherichia coli* (strain K-12)

C:Species: *Escherichia coli*

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: C64843

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64843

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-212 <BLAT>

A:Cross-references: GB:AE000203; GB:U00096; NID:g1787248; PIDN:AAC74098.1; PID:g17872

A:Experimental source: strain K-12, substrain MO1655

C:Genetics:

A:Gene: ycdC

A:Keywords: DNA binding; transcription regulation

F:33-58/Region: helix-turn-helix motif

Query Match

Best Local Similarity 64.3%; Score 18; DB 2; Length 212;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12

DB 20 KKAIISSALD 29

RESULT 11

B64080

hypothetical protein HI0601 - *Haemophilus influenzae* (strain Rd KW20)

C:Species: *Haemophilus influenzae*

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C:Accession: B64080

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, G.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Feldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: B64080

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-217 <TIGR>

A:Cross-references: GB:U32741; GB:I42023; NID:g1573582; PIDN:AAC22258.1; PID:g1573592

Query Match

Best Local Similarity 64.3%; Score 18; DB 2; Length 217;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXXXXXXLD 12

DB 161 KKSGSGATLD 170

RESULT 12

T14770

hypothetical protein DKFZP566E144.1 - human

C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000
 C:Accession: T14770
 R:Boecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: 218182
 A:Accession: T14770
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-237 <BL0>
 A:Cross-References: EMBL:AL110239
 A:Experimental source: fetal kidney; clone DKFZp566E144
 C:Genetics:
 A:Note: DKFZp566E144.1
 C:Superfamily: human conserved hypothetical protein DKFZp566E144.1

Query Match
 Best Local Similarity 64.3%; Score 18; DB 2; Length 237;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXXLD 12
 || ||
 DB 189 KKAASHRALD 198

RESULT 13
 S01924
 hypothetical protein 6 - Chlamydia trachomatis plasmids
 N:Alternate names: hypothetical protein P-10
 C:Species: Chlamydia trachomatis
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Oct-1999
 C:Accession: S01924; S00794
 R:Comanducci, M.; Ricci, S.; Ratti, G.
 M.Ol. Microbiol. 2, 531-538, 1988
 A:Title: The structure of a plasmid of Chlamydia trachomatis believed to be required for
 A:Reference number: S01920; MUID:89013895; PMID:2845228
 A:Accession: S01924
 A:Molecule type: DNA
 A:Residues: 1-247 <COM>
 A:Cross-References: EMBL:X07547; NID:940730; PIDN:CAA30426.1; PID:9581014
 A:Experimental source: plasmid pCHL1
 R:Note: the authors translated the initiation codon GTG for residue 1 as Val
 R:Hatt, C.; Ward, M.E.; Clarke, I.N.
 Nucleic Acids Res. 16, 4053-4067, 1988
 A:Title: Analysis of the entire nucleotide sequence of the cryptic plasmid of Chlamydia
 A:Reference number: S00788; MUID:8823398; PMID:2836808
 A:Accession: S00794
 A:Molecule type: DNA
 A:Residues: 175-247 <HAT>
 A:Cross-References: EMBL:X06707
 A:Experimental source: plasmid pLGV440
 C:Genetics:
 A:Genome: plasmid
 A:Start codon: GTG

Query Match
 Best Local Similarity 64.3%; Score 18; DB 2; Length 247;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXXLD 12
 || ||
 DB 13 KKNOTASLD 22

RESULT 14
 F37386
 hypothetical protein 6 - Chlamydia trachomatis (serotype D) plasmid pCHL1
 C:Species: Chlamydia trachomatis
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Feb-1994
 C:Accession: F37386
 R:Comanducci, M.; Ricci, S.; Cevenini, R.; Ratti, G.
 plasmid 23, 149-154, 1990
 A:Title: Diversity of the Chlamydia trachomatis common plasmid in biovars with different

A:Reference number: A37386; MUID:90301796; PMID:2194229
 A:Accession: F37386
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-247 <COM>
 A:Cross-References: GB:J03321
 C:Genetics:
 A:Genome: plasmid

Query Match
 Best Local Similarity 64.3%; Score 18; DB 2; Length 247;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXXLD 12
 || ||
 DB 13 KKNOTASLD 22

RESULT 15
 AB3091
 hypothetical protein Atu4350 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AB3091
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavain, T.; Levy, R.; Li, M.; McCl
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AB3091
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-278 <KUP>
 A:Cross-References: GB:AE008689; PIDN:AAL45144.1; PID:917742817; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4350
 A:Map position: linear chromosome

Query Match
 Best Local Similarity 64.3%; Score 18; DB 2; Length 278;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXXLD 12
 || ||
 DB 184 KKLATHTLD 193

Search completed: June 5, 2003, 15:34:01
 Job time : 12.8182 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:34:07 ; Search time 7.81818 Seconds
(without alignments)
63.661 Million cell updates/sec

Title: US-09-150-947f-17
Perfect score: 28
Sequence: 1 XXXXXXXXXXXXLD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	64.3	100 1	RRL4_MARPO
2	18	64.3	152 1	NIJ1_HUMAN
3	18	64.3	152 1	NIJ1_MOUSE
4	18	64.3	152 1	NIJ1_RAT
5	18	64.3	169 1	YML3_PASTE
6	18	64.3	212 1	YCDC_ECOLI
7	18	64.3	217 1	TFOX_HAEIN
8	18	64.3	237 1	ORN_HUMAN
9	18	64.3	247 1	GP6D_CHLTR
10	18	64.3	344 1	FLC1_PROMI
11	18	64.3	365 1	Y349_MYCPN
12	18	64.3	413 1	ARP3_SCHPO
13	18	64.3	427 1	ARP3_SCHPO
14	18	64.3	477 1	XRNA_STRLI
15	18	64.3	837 1	YL34_YEAST
16	18	64.3	1279 1	BCNR_CHLVI
17	17	60.7	81 1	EX7S_PASMU
18	17	60.7	118 1	YQ93_CAEEL
19	17	60.7	142 1	NIJ2_HUMAN
20	17	60.7	143 1	NIJ2_MOUSE
21	17	60.7	144 1	NIJ2_RAT
22	17	60.7	147 1	RL15_MYCGA
23	17	60.7	156 1	ATPX_OPOSI
24	17	60.7	185 1	3MGA_HAEIN
25	17	60.7	186 1	YABF_BACSU
26	17	60.7	211 1	ORN_DROME
27	17	60.7	217 1	GRPE_MYCGE
28	17	60.7	233 1	GRPE_MYCGE
29	17	60.7	234 1	TSST_STPAU
30	17	60.7	256 1	YB32_MYCPN
31	17	60.7	266 1	ETC2_STPAU
32	17	60.7	266 1	ETC2_STPAU
33	17	60.7	266 1	ETC3_STPAU

34	17	60.7	272 1	TRDB_CAMJE	Q9P12 campylobact
35	17	60.7	276 1	MYO1_ONCMY	Q91205 oncorhynch
36	17	60.7	307 1	ERA_NEIMA	Q91422 neisaria m
37	17	60.7	307 1	ERA_NEIMA	Q91422 neisaria m
38	17	60.7	347 1	YAB9_MYCPN	P75593 mycoplasma
39	17	60.7	363 1	LE3A_ASPPG	P87236 aspergillus
40	17	60.7	368 1	DXR_HELPJ	Q9ZML6 helicobacte
41	17	60.7	390 1	CNX2_ARATH	Q39055 arabidopsi
42	17	60.7	399 1	Y199_ARCFU	Q28380 archaeglob
43	17	60.7	413 1	YB44_MYCPN	P75142 mycoplasma
44	17	60.7	457 1	PRC2_STRGR	P52320 streptomyc
45	17	60.7	467 1	LEU2_ANASP	Q8YX02 anabaena sp

ALIGNMENTS

RESULT 1
RRL4_MARPO STANDARD; PRT; 100 AA.
ID AC P06370;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chloroplast 30S ribosomal protein S14.
GN RPS14.
OS Marchantia polymorpha (Liverwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC Marchantiopsida; Marchantiales; Marchantiaaceae; Marchantia.
OC Marchantiaceae; Marchantia.
OX NCBI_TaxID=3197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087956; PubMed=6393057;
RA Ohnuma K., Inokuchi H., Ohnuma K., Ozeki H.;
RT "Nucleotide sequence of Marchantia polymorpha chloroplast DNA: a region possibly encoding three tRNAs and three proteins including a homologue of E. coli ribosomal protein S14.";
RL Nucleic Acids Res. 12:9551-9565(1984).
RN [2]
RP SEQUENCE FROM N.A.
RA Ohnuma K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S., Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H., Ozeki H.;
RT "Chloroplast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA.";
RL Nature 332:572-574(1986).
CC -1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: X01647; CA25805.1; -;
DR EMBL: X04465; CA28083.1; -;
DR PIR: A02733; R3LV14.
DR InterPro: IPR001209; Ribosomal_S14.
DR Pfam: PF00253; Ribosomal_S14; 1.
DR PROSITE: PS00527; RIBOSOMAL_S14; 1.
KW RIBOSOMAL protein; Chloroplast.
SQ SEQUENCE 100 AA; 11880 MW; 5AB14F480963EEB0 CRC64;
Query Match 64.3%; Score 18; DB 1; Length 100;
Best Local Similarity 40.0%; Pred. No. 4.4;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
3 XXXXXXXXLD 12
|||

DB	29	KK1ETSSLD	38
RESULT 2			
NIJ1_HUMAN	STANDARD:	PRT:	152 AA.
ID	NIJ1_HUMAN		
AC	Q92982; Q9BT07;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Ninjurin 1 (Nerve injury-induced protein 1).		
GN	NINJ1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96374367; PubMed=8780658;		
RA	Araki T., Milbrandt J.;		
RT	"Ninjurin, a novel adhesion molecule, is induced by nerve injury and promotes axonal growth."		
RL	Neuron 17:353-361(1996).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98126436; PubMed=9465296;		
RA	Chadwick B.P., Heath S.K., Williamson J., Obermayr F., Patel L.,		
RA	Sheer D., Fritschauf A.-M.;		
RT	"The human homologue of the ninjurin gene maps to the candidate region of hereditary sensory neuropathy type I (HSNI)."		
RL	Genomics 47:58-63(1998).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RP	TISSUE=Lung;		
RC	Strausberg R.;		
RA	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
RA	[4]		
RP	CHARACTERIZATION.		
RX	MEDLINE=97407927; PubMed=9261151;		
RA	Araki T., Zimonjic D.B., Popescu N.C., Milbrandt J.;		
RT	"Mechanism of homophilic binding mediated by ninjurin, a novel widely expressed adhesion molecule."		
RL	J. Biol. Chem. 272:21373-21380(1997).		
CC	-I- FUNCTION: HOMOPHILIC CELL ADHESION MOLECULE THAT PROMOTES AXONAL GROWTH. MAY PLAY A ROLE IN NERVE REGENERATION AND IN THE FORMATION AND FUNCTION OF OTHER TISSUES. CELL ADHESION REQUIRES DIVALENT CATIONS.		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-I- TISSUE SPECIFICITY: WIDELY EXPRESSED IN BOTH ADULT AND EMBRYONIC TISSUES, PRIMARILY THOSE OF EPITHELIAL ORIGIN.		
CC	-I- INDUCTION: BY NERVE INJURY BOTH IN DORSAL ROOT GANGLION NEURONS AND IN SCHWANN CELLS.		
CC	-I- SIMILARITY: BELONGS TO THE NINJURIN FAMILY.		
CC	-----		
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CC	-----		
DR	EMBL; U72661; AAB17560.1; -		
DR	EMBL; AF015112; AAC14593.1; -		
DR	EMBL; AF029251; AAC39574.1; -		
DR	EMBL; BC004440; AAH04440.1; -		
DR	Gene; HGNC:7824; NINJ1.		
DR	MI: 602062; -		
KW	Cell adhesion; Transmembrane.		
FT	DOMAIN 1 80		
FT	TRANSMEM 81 101		
FT	DOMAIN 102 120		
FT	TRANSMEM 121 141		
FT	POTENTIAL. CYTOPLASMIC (POTENTIAL). POTENTIAL.		

FT	DOMAIN	142	152	EXTRACELLULAR (POTENTIAL).
FT	CONFLICT	110	110	D -> A (IN REF.3)
SD	SEQUENCE	152 AA;	16389 MW;	FEACAD8001597855 CRC64;
Query Match				
Best Local Similarity		40.3%;	Score 18;	DB 1; Length 152;
Matches		4; Conservative	0;	Mismatches 6; Indels 0; Gaps 0
OY	3 KKKXXXXXLD 12			
DB	44 KKSAAESMLD 53			
RESULT 3				
ID	NINJ_MOUSE	STANDARD;	PRT;	152 AA.
AC	070131.			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ninjurin 1 (Nerve Injury-Induced protein 1).			
GN	NINJ1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
[1]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98126436; PubMed=9465296;			
RA	Chadwick B.P., Heath S.K., Williamson J., Obermayr F., Patel L.,			
RA	Sheer D., Fritschau A.M.;			
RT	"The human homologue of the ninjurin gene maps to the candidate region			
RT	of hereditary sensory neuropathy type I (HSNI).";			
RL	Genomics 47:58-63(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Moon A.R., Kim J.W., Hong Y.M., Oh G.T., Chang S.Y., Lee K.S.,			
RA	Choe I.S.;			
RT	"Mus musculus ninjurin genomic DNA.";			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: HOMOPHILIC CELL ADHESION MOLECULE THAT PROMOTES AXONAL			
CC	GROWTH. MAY PLAY A ROLE IN NERVE REGENERATION AND IN THE FORMATION			
CC	AND FUNCTION OF OTHER TISSUES. CELL ADHESION REQUIRES DIVALENT			
CC	CATIONS (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- INDUCTION: BY NERVE INJURY.			
CC	-1- SIMILARITY: BELONGS TO THE NINJURIN FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; U91513; AAC14594.1; -.			
DR	EMBL; AF219626; AAG32161.1; -.			
DR	MGI; MGI:1196617; NINJ1.			
KW	Cell adhesion; Transmembrane.			
FT	DOMAIN	1	79	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	80	100	POTENTIAL.
FT	DOMAIN	101	120	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	121	141	POTENTIAL.
FT	DOMAIN	142	152	EXTRACELLULAR (POTENTIAL).
SO	SEQUENCE	152 AA;	16555 MW;	E261CB447BC0A2E6 CRC64;
Query Match				
Best Local Similarity		64.3%;	Score 18;	DB 1; Length 152;
Matches		4; Conservative	0;	Mismatches 6; Indels 0; Gaps 0
OY	3 KKKXXXXXLD 12			
DB	44 KKSAAESMLD 53			

```

RX MEDLINE-90174913; PubMed-2308823;
RA Pritchard A.E., Sellhammer J.T., Mahalingam R., Sable C.L.,
RT Venuti S.E., Cummings D.J.;
RL "Nucleotide sequence of the mitochondrial genome of Parametium.";
CC -----
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CC -----
DR EMBL; X15917; CAA34057.1; -
DR PIR; S07748; S07748.
KM Hypothetical protein; Mitochondrion.
SQ SEQUENCE 169 AA; 20303 MM; D991AD99ABEA174 CRC64;

Query Match 64.3%; Score 18; DB 1; Length 169;
Best Local Similarity 40.0%; Pred. No. 7.2;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
Db 36 KKTSTYSKLD 45
  ||
  ||

RESULT 6
YCDC_ECOLI STANDARD; PRT; 212 AA.
AC P75899;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator ycdc.
GN YCDC OR B1013.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
CX NCBI_Taxid-562;
XX [1]
RN SEQUENCE FROM N.A.
RP STRAIN-K12 / MG1655;
RX MEDLINE-9742617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Siao Y.;
RL "The complete genome sequence of Escherichia coli K-12.";
RT Science 277:1453-1474(1997).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-K12;
RX MEDLINE-97061202; PubMed-8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishio Y., Saito N.,
RA Stempel G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiiuchi T.;
RL "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RN DNA Res. 3:137-155(1996).
RL -1 STIMULATORY; BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----

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CC NUCLEOTIDES IN LENGTH) SINGLE-STRANDED RNA AND DNA OLIGOMERS. MAY
 CC HAVE A ROLE FOR CELLULAR NUCLEOTIDE RECYCLING.
 CC -1- COFACTOR: MANGANESE.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (LONG ISOFORM) AND NUCLEAR
 CC (SHORT ISOFORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/SEN-ALPHA (SHOWN
 CC HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE OLIGORIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF151872; A034109.1; -
 CC EMBL; AL110239; CAB53690.1; -
 CC InterPro: IPR000520; Exonuclease.
 CC Pfam: PF00929; Exonuclease: 1.
 CC SMART: SM00479; EXOIII.1.
 CC K01001; Exonuclease; Nuclease; Mitochondrion; Transit peptide;
 CC Nuclear protein; Manganese; Alternative splicing.
 CC TRANSIT 1 237
 CC CHAIN ? 237
 CC FT ACT_SITE 164 164 POTENTIAL.
 CC FT VARSPIC 1 38 MISSING (IN ISOFORM 2).
 CC FT MTAGN 168 168 D->A: ABOLISHES ACTIVITY.
 CC FT CONFLICT 103 103 R->K (IN REF. 1).
 CC SQ SEQUENCE 237 AA; 26861 MW; BF093A89078C13BF CRC64;
 CC
 CC Query Match 64.3%; Score 18; DB 1; Length 237;
 CC Best Local Similarity 40.0%; Pred. No. 10;
 CC Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 CC
 CC QY 3 KKKXXXXXLD 12
 CC Db 189 KKAASHRALD 198
 CC
 CC RESULT 9
 CC GP6D_CHLTR STANDARD; PRT; 247 AA.
 CC ID GP6D_CHLTR STANDARD; PRT; 247 AA.
 CC AC P10560; P08787; Q46433;
 CC DT 01-NOV-1988 (Rel. 09, Created)
 CC DT 01-JUN-1989 (Rel. 11, Last sequence update)
 CC DT 15-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Virulence plasmid protein pGP6-D (Protein P-10).
 CC OS Chlamydia trachomatis.
 CC OG Plasmid pLG440, Plasmid pCHL1, and Plasmid pCTT1.
 CC OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 CC OX NCBI_TaxID-813;
 CC RN
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-L2/434/Bu; PLASMID-PLGV440;
 CC RX MEDLINE-89013895; PubMed-2845228;
 CC RA Comanducci M., Ricci S., Ratti G.;
 CC "The structure of a plasmid of Chlamydia trachomatis believed to be
 CC required for growth within mammalian cells.";
 CC Mol. Microbiol. 2:531-538(1988).
 CC RL
 CC RM
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-L1/440/LN; PLASMID-PLGV440;
 CC RX MEDLINE-8823398; PubMed-2836808;
 CC RA Hatt C., Ward M.E., Clarke I.N.;
 CC "Analysis of the entire nucleotide sequence of the cryptic plasmid of
 CC Chlamydia trachomatis serovar L1. Evidence for involvement in DNA
 CC replication.";
 CC J. Bacteriol. 16:4053-4067(1988).
 CC RT
 CC RN
 CC RP SEQUENCE FROM N.A.

CC STRAIN-G0/86 / Serotype D; PLASMID-pCHL1;
 CC MEDLINE-90301796; PubMed-2194229;
 CC RA Comanducci M., Ricci S., Cevenini R., Ratti G.;
 CC "Diversity of the Chlamydia trachomatis common plasmid in biovars
 CC RT with different pathogenicity.";
 CC RL Plasmid 23:149-154(1990).
 CC RM
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-Serotype B; PLASMID-pCTT1;
 CC RX MEDLINE-8817106; PubMed-3444859;
 CC RA Sriprakash K.S., Macavoy E.S.;
 CC "Characterization and sequence of a plasmid from the trachoma biovar
 CC RT of Chlamydia trachomatis.";
 CC RL Plasmid 18:205-214(1987).
 CC CC -1- MISCELLANEOUS: PG6-D IS REQUIRED FOR GROWTH WITHIN MAMMALIAN
 CC CELLS.
 CC CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF PLASMID PLGV440.
 CC CC -1- SIMILARITY: BELONGS TO THE UPF0137 (PG6-D) FAMILY.
 CC CC -----
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 CC -----
 CC EMBL; X07547; CA30426.1; -
 CC EMBL; X06707; CA29897.1; -
 CC EMBL; J03321; AA91574.1; -
 CC EMBL; M19487; AAB02591.1; -
 CC DR PIR: S01924; A01924.
 CC DR PIR: S00794; S00794.
 CC DR InterPro: IPR005350; UPF0137.
 CC DR Pfam: PF03677; UPF0137; 1.
 CC K01001; Plasmid.
 CC FT VARIANT 9 9 N->D (IN PLASMIDS PCHL1 AND PCTT1).
 CC FT VARIANT 47 47 Q->R (IN PLASMIDS PCHL1 AND PCTT1).
 CC FT VARIANT 183 186 VLQD->CWTE (IN PLASMID PCTT1).
 CC FT VARIANT 194 194 K->T (IN PLASMID PCTT1).
 CC FT VARIANT 205 205 S->L (IN PLASMID PCTT1).
 CC FT VARIANT 222 222 M->I (IN PLASMID PCTT1).
 CC SQ SEQUENCE 247 AA; 28307 MW; F1FA1F29307C221 CRC64;
 CC
 CC Query Match 64.3%; Score 18; DB 1; Length 247;
 CC Best Local Similarity 40.0%; Pred. No. 10;
 CC Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 CC
 CC QY 3 KKKXXXXXLD 12
 CC Db 13 KKNQTAASLD 22
 CC
 CC RESULT 10
 CC VPQ_BPP2 STANDARD; PRT; 344 AA.
 CC ID VPQ_BPP2 STANDARD; PRT; 344 AA.
 CC AC P25480;
 CC DT 01-MAY-1992 (Rel. 22, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
 CC DE Presumed portal vertex protein (GPO).
 CC GN
 CC OS Bacteriophage P2.
 CC OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 CC CC P2-like viruses.
 CC OX NCBI_TaxID-10679;
 CC RN
 CC RP SEQUENCE FROM N.A.
 CC RC MEDLINE-92115571; PubMed-1837355;
 CC RA Linderoth N.A., Ziermann R., Hagggaard-Ljungquist E., Christie G.E.,
 CC "Nucleotide sequence of the DNA packaging and capsid synthesis genes
 CC of bacteriophage P2.";
 CC J. Virol. 67:100-106(1993).

RL Nucleic Acids Res. 19:7207-7214(1991).
 CC -1- FUNCTION: THE Q, P AND M PROTEINS ARE NEEDED TO PACKAGE DNA INTO
 CC PROHEADS AND FOR THE CONVERSION OF PROHEADS TO CAPSID.
 CC -1- SIMILARITY: STRONG, TO PHAGE HP1 PROTEIN ORF15 AND TO THE E. COLI
 CC HYPOTHETICAL 36.8 kDa PROTEIN (ORF5) IN RETRON EC67.
 CC -----
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 CC -----
 DR EMBL; AF063097; AAD03268.1; -
 DR PIR; S16410; S16410.
 DR PIR; S22796; S22796.
 KM Capsid assembly.
 SQ SEQUENCE 344 AA; 39114 MW; FAD61987530029A7 CRC64;
 Query Match 64.3%; Score 18; DB 1; Length 344;
 Best Local Similarity 40.0%; Pred. No. 14;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 3 KXXXXXXD 12
 DB 270 KKASADLD 279
 RESULT 11
 ID FLCL1_PROMT STANDARD; PRT; 365 AA.
 AC P42272;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Flagellin 1.
 GN FLIC1.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.
 OX NCBI_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-29.
 RC STRAIN-BB2000;
 RX MEDLINE-95011656; PubMed-7926835;
 RA Belas R., Flaherty D.;
 RT "Sequence and genetic analysis of multiple flagellin-encoding genes
 RT from Proteus mirabilis.";
 RL Gene 148:33-41(1994).
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
 CC -1- INDUCTION: ALTHOUGH SWIMMER CELLS HAVE ONLY A FEW FLAGELLA, THE
 CC ELONGATED SPARGER CELLS ARE PROPOSEDLY COVERED BY THOUSANDS OF NEW
 CC FLAGELLA SYNTHESIZED SPECIFICALLY IN RESPONSE TO GROWTH ON
 CC SURFACES OR IN HIGHLY VISCOUS LIQUIDS.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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 CC -----
 DR EMBL; AF221596; AAA62396.1; -
 DR InterPro; IPR001492; Flagellin.
 DR InterPro; IPR001029; Flagellin_C.
 DR Pfam; PF00669; Flagellin_N; 1.
 DR Pfam; PF00700; Flagellin_C; 1.
 DR PRINTS; PR00207; FLAGELLIN.
 DR Prodom; PD000316; Flagellin_C; 1.

KW Flagella; Multigene family.
 SQ SEQUENCE 365 AA; 39093 MW; 2A23106F040DB522 CRC64;
 Query Match 64.3%; Score 18; DB 1; Length 365;
 Best Local Similarity 40.0%; Pred. No. 15;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 3 KXXXXXXD 12
 DB 197 KRINAATLD 206
 RESULT 12
 ID Y349_MYCPN STANDARD; PRT; 413 AA.
 AC P75253;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG349 homolog (G12_orf413).
 GN MPN525 OR MP317.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE-97105885; PubMed-8948633;
 RA Himmelfreith R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -----
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 CC -----
 DR EMBL; AE000029; AAB95965.1; -
 DR Hypothetical protein; Complete proteome.
 KM SEQUENCE 413 AA; 48246 MW; AACPC2C9802316P23 CRC64;
 Query Match 64.3%; Score 18; DB 1; Length 413;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 3 KXXXXXXD 12
 DB 10 KKATSPSCGD 19
 RESULT 13
 ID ARP3_SCHPO STANDARD; PRT; 427 AA.
 AC P32390;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Actin-like protein 3.
 GN ACT2 OR SPAC630.03.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92108083; PubMed-1729722;
 RA Lees-Miller J.P., Henry G., Helfman D.M.;

* Identification of act2, an essential gene in the fission yeast Schizosaccharomyces pombe that encodes a protein related to actin. [2]
Proc. Natl. Acad. Sci. U.S.A. 89:80-83(1992).

RP SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE-21648401; PubMed-11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabblowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grymonprez B., Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wandutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Kottler S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerritelli L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Spharovsky G.V., Ussery D., Barrett B.G., Nurse P.;
RT The genome sequence of Schizosaccharomyces pombe.*;
RL Nature 415:871-880(2002).

-1- FUNCTION: PART OF A COMPLEX IMPLICATED IN THE CONTROL OF ACTIN POLYMERIZATION IN CELLS (BY SIMILARITY). MAY BE INVOLVED IN CYTOKINESIS.
CC -1- SUBUNIT: BELONGS TO A COMPLEX COMPOSED OF ARP2, ARP3, P41-ARC, P34-ARC, P21-ARC, P20-ARC AND P16-ARC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY. ARP3 SUBFAMILY.
CC
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CC
CC
CC EMBL: M81068; -; NOT_ANNOTATED_CDS.
DR EMBL: AL109832; CAB52725.1; -;
DR PIR: A41790; A41790.
DR InterPro: IPR004000; Actin_like.
DR Pfam: PF000022; actin; 1.
DR SMART: SM00268; ACTIN; 1.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein; Cytoskeleton.
SQ SEQUENCE 427 AA; 47373 MW; C7909FEE544789B CRC64;

Query Match 64.3%; Score 18; DB 1; Length 427;
Best Local Similarity 40.0%; Pred. NO. 17;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKKXXXXD 12
Db 82 KKASAGYSD 91

RESULT 14
XYNA_STRLI STANDARD; PRT; 477 AA.
AC P26514; P96464;
DT 01-APR-1992 (Rel. 23, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylosylase A precursor (EC 3.2.1.8) (Xylanase A)
GN (1,4-beta-D-xylosyl xylanohydrolase A).
OS XLANA.
OC Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-92.
RC STRAIN-66 / 1326;
RX MEDLINE-92077439; PubMed-1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces lividans.";
RL Gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 20 AND 140-141.
RC STRAIN-66 / 1326;
RA Shareck F.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.
RX MEDLINE-94342232; PubMed-8063693;
RA Derwenda U., Swenson L., Green R., Wei Y.Y., Morosoli R., Shareck F., Kluepfel D., Derwenda Z.S.;
RT Crystal structure, at 2.6-A resolution, of the Streptomyces lividans xylanase A, a member of the F family of beta-1,4-D-glucanases.";
RL J. Biol. Chem. 269:20811-20814(1994).

-1- FUNCTION: CONTRIBUTES TO HYDROLYSE Hemicellulose, THE MAJOR COMPONENT OF PLANT CELL-WALLS. XLAN AND XLAN SEEM TO ACT SEPARATELY ON THE SUBSTRATE TO YIELD xylobiose AND xylose AS CARBON SOURCES.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
CC
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CC
CC
CC EMBL: M64551; AAC26525.1; -;
DR PIR: JS0589; JS0589.
DR PDB: 1XAS; 3I-MAY-95.
DR InterPro: IPR001000; Glyco_hydro_10.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00652; Ricin_B_lectin; 3.
DR PRINTS: PR00134; GLYHYDRLASE10.
DR SMART: SM00458; RICIN; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00231; RICIN_B_LLECTIN; 1.
KW Xylan degradation; Hydrolyase; Glycosidase; Signal; Lectin; 3D-structure.
FT SIGNAL 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
FT ACT_SITE 169 169 PROTON DONOR.
FT ACT_SITE 277 277 NUCLEOPHILE.
SQ SEQUENCE 477 AA; 51162 MW; E14A7FE37BDC68CC CRC64;

Query Match 64.3%; Score 18; DB 1; Length 477;
Best Local Similarity 40.0%; Pred. NO. 19;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 330 KKAAYTAVLD 339

RESULT 15

YL34_YEAST
ID YL34_YEAST STANDARD; PRT; 837 AA.
AC 007844;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 93.1 kDa protein YL034C.
GN YL034C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;

RP [1]
RA Duesterhoeft A., Floeth M., Heuss-Neltzel D., Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.

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DR EMBL: Z73139; CAA97483.1; -.
DR SGD: S0003957; YL034C.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003599; AAA_ATPase-centr.
DR InterPro: IPR003960; AAA_sub.
DR Pfam: PF00004; AAA; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00674; AAA; 1.
KW Hypothetical protein: ATP-binding. Repeat.
FT NP_BIND 246 253 ATP (POTENTIAL).
FT NP_BIND 574 581 ATP (POTENTIAL).
SQ SEQUENCE 837 AA; 93069 MW; 13528B9D0987103 CRC64;

Query Match 64.3%; Score 18; DB 1; Length 837;
Best Local Similarity 40.0%; Pred. NO. 33;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 7 KKNSTSSLD 16

Search completed: June 5, 2003, 15:56:35
Job time : 8.81818 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:32:58 ; Search time 34.9091 Seconds
(without alignments)
70.829 Million cell updates/sec

```
Title: US-09-150-947F-17
Perfect score: 28
Sequence: 1 XXXXXXXXXXXXLD 12
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

```

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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :

SPRMBL.21.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertebrate.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archaeap.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	67.9	284	3	Q9URX9	Q9URX9 schizosacch
2	19	67.9	378	10	Q9ZVH8	Q9ZVH8 arabidopsist
3	19	67.9	378	10	Q8VXZ6	Q8VXZ6 arabidopsist
4	19	67.9	1365	12	Q37174	Q37174 bamboo moss
5	19	67.9	1365	12	Q65005	Q65005 bamboo moss
6	19	67.9	1365	12	Q8UZ48	Q8UZ48 bamboo moss
7	18	64.3	46	2	Q9ZG37	Q9ZG37 chlamydia t
8	18	64.3	108	2	Q8RTG3	Q8RTG3 escherichia
9	18	64.3	153	2	Q9ANS7	Q9ANS7 vibrio harv
10	18	64.3	161	4	Q8WUV5	Q8WUV5 homo sapien
11	18	64.3	160	4	Q9RL32	Q9RL32 vibrio chol
12	18	64.3	171	10	Q04541	Q04541 arabidopsist
13	18	64.3	205	11	Q9D854	Q9D854 mus musculu
14	18	64.3	212	16	Q8X4Z7	Q8X4Z7 escherichia
15	18	64.3	213	5	Q96609	Q96609 entamoeba h
16	18	64.3	276	8	P92729	P92729 paramecium

17	18	44.3	278	16	08U709
18	18	64.3	292	11	08R1E2
19	18	64.3	357	15	09OFU8
19	18	64.3	371	15	09OKI9
21	18	64.3	376	12	056872
22	18	64.3	385	15	098RJ3
23	18	64.3	543	5	04I130
24	18	64.3	663	8	09MJ69
25	18	64.3	716	2	09REV3
26	18	64.3	716	2	046317
27	18	64.3	716	2	093QC9
28	18	64.3	765	4	0969N7
29	18	64.3	765	4	096GQ7
30	18	64.3	796	4	096L97
31	18	64.3	841	2	044207
32	18	64.3	858	5	021853
33	18	64.3	863	16	097LNO
34	18	64.3	954	5	09G0I5
35	18	64.3	969	5	09U022
36	18	64.3	1032	5	019818
37	18	64.3	1035	5	021380
38	18	64.3	1117	5	08TIU6
39	18	64.3	1271	2	093SV9
40	17	60.7	72	5	096726
41	17	60.7	109	17	028686
42	17	60.7	119	17	0975E7
43	17	60.7	137	16	09PKF9
44	17	60.7	137	16	084238
45	17	60.7	145	5	08SWF8
					08U709 agrobacteri
					08r1e2 mus musculu
					09ofu8 human immun
					09okI9 human immun
					056872 gallid herp
					098RJ3 human immun
					04I130 caenorhabd
					09mj69 physarum po
					09rev3 carnobacter
					046317 carnobacter
					093qc9 carnobacter
					0969n7 homo sapien
					096gq7 homo sapien
					096l97 homo sapien
					044207 agrobacteri
					021853 caenorhabd
					097lno clostridium
					09g0i5 giardia lam
					09u022 giardia lam
					019818 caenorhabd
					021380 caenorhabd
					08tiU6 dictyostel
					093sv9 chlorobium
					096726 lutzomyia l
					028686 archaeoglob
					0975e7 sulfoblob
					09pkf9 chlamydia m
					084238 chlamydia t
					08swf8 encephalito

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ALIGNMENTS

RESULT 1
Q9URX9 ID Q9URX9 PRELIMINARY; PRT; 284 AA.
AC Q9URX9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DT Hypothetical 31.9 kDa protein C890.05 in chromosome I.
GM SPC890.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Saunders D., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133498; CAB63496.1; -
DR InterPro: IPR000467; G_patch.
DR Pfam; PF01585; G_patch; 1.
DR SMART; SM00443; G_patch; 1.
DR Hypothetical protein.
RW DOMAIN 197 201 POLY-LYS.
FT DOMAIN 225 233 POLY-LYS.
FT FT
SQ SEQUENCE 284 AA; 31878 MW; A10F14DDE2FA0235 CRC64;

Query Match 67.9%; Score 19; DB 3; Length 284;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

CY 3 KKKKXXXXLD 12
||
||
DB 179 KKTSTGSALD 188

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ID 092VH8 PRELIMINARY; PRT; 378 AA.
AC 092VH8:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative elongation factor.
GN AR2638560
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Bentto M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldguy A.V.,
RA Buell C.R., Ketchum K.A., Lee J.U., Konning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umeyam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Greasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana";
RL Nature 402:761-768 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC005499; AAC67362.1;
DR HSBP; F23193; ITT1.
DR InterPro; IPR001222; TFIIS.
DR InterPro; IPR003618; TFS2_centre.
DR InterPro; IPR003617; TFS2_N.
DR Pfam; PF01096; TFIIS; 1.
DR SMART; SM00510; TFS2M; 1.
DR SMART; SM00509; TFS2N; 1.
DR SMART; SM00440; znf_C2C2; 1.
DR PROSITE; PS00466; TFIIS; 1.
KW Elongation factor.
SQ SEQUENCE 378 AA; 41979 MW; 9A176DC31FA8885 CRC64;

Query Match 67.9%; Score 19; DB 10; Length 378;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
DB 13 KKADAAALD 22

RESULT 3
OBVX26 PRELIMINARY; PRT; 378 AA.
AC 08VX26:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative elongation factor.
GN AT2638560.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Ban J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

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RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Natusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shin P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene At2g38560 (GI:15224901)";
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF074322; AAL67018.1;
DR InterPro; IPR001222; TFIIS.
DR InterPro; IPR003618; TFS2_centre.
DR InterPro; IPR003617; TFS2_N.
DR Pfam; PF01096; TFIIS; 1.
DR SMART; SM00510; TFS2M; 1.
DR SMART; SM00509; TFS2N; 1.
DR SMART; SM00440; znf_C2C2; 1.
DR PROSITE; PS00466; TFIIS; UNKNOWN_1.
KW Elongation factor.
SQ SEQUENCE 378 AA; 42011 MW; 045EE924FBD9CDB CRC64;

Query Match 67.9%; Score 19; DB 10; Length 378;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
DB 13 KKADAAALD 22

RESULT 4
O37174 PRELIMINARY; PRT; 1365 AA.
AC 037174:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Replicase.
OS Bamboo mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=35286;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S;
RA Liao J.T., Hsu Y.H.;
RT "Full-length sequence of infectious bamboo mosaic virus genomic RNA.";
RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF018156; AAB70562.1;
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR006066; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
SQ SEQUENCE 1365 AA; 155219 MW; CA54D8F5997F158A CRC64;

Query Match 67.9%; Score 19; DB 12; Length 1365;
Best Local Similarity 40.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
DB 1302 KKTATATVALD 1311

RESULT 5
O65005 PRELIMINARY; PRT; 1365 AA.
AC 065005:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF1-155k.
OS Bamboo mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=35286;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-BAMV-O;
 RA Hsu Y.-H.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BAMV-O;
 RX MEDLINE-94358760; PubMed-8077956;
 RA Lin N., Lin B., Lo N., Hu C., Chow T., Hsu Y.;
 RT "Nucleotide sequence of the genomic RNA of bamboo mosaic potexvirus.";
 RL J. Gen. Virol. 75:2513-2518(1994).
 DR EMBL: D26017; BAA05033.1; -;
 DR Interpro: IPR001788; RNA_dep_RNAPol2.
 DR Interpro: IPR000606; Viral_helicase1.
 DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
 DR Pfam: PF01443; Viral_helicase1; 1.
 SQ SEQUENCE 1365 AA; 155129 MW; 35449D5E80026633 CRC64;

Query Match 67.9%; Score 19; DB 12; Length 1365;
 Best Local Similarity 40.0%; Pred. No. 79;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
 DB 1302 KKTATAYALD 1311

RESULT 6
 Q8UZ48 PRELIMINARY; PRT; 1365 AA.
 AC 08UZ48;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative, putative, putative, putative, and putative genes.
 OS Bamboo mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 OX NCBI_TaxID=35286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BAMV-V;
 RA Yang C.-C., Liu J.-S., Lin C.-P., Lin N.-S.;
 RT "Nucleotide sequence and phylogenetic analysis of a bamboo mosaic
 RT potexvirus isolate from common bamboo (Bambusa vulgaris McClure).";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L77962; AAL40030.1; -;
 DR Interpro: IPR001788; RNA_dep_RNAPol2.
 DR Interpro: IPR000606; Viral_helicase1.
 DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
 DR Pfam: PF01443; Viral_helicase1; 1.
 SQ SEQUENCE 1365 AA; 155222 MW; B542C00E2ECFC990 CRC64;

Query Match 67.9%; Score 19; DB 12; Length 1365;
 Best Local Similarity 40.0%; Pred. No. 79;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
 DB 1302 KKTATAYALD 1311

RESULT 7
 Q9ZG37 PRELIMINARY; PRT; 46 AA.
 AC 09ZG37;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 5.2 kDa protein (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RL NCBI_TaxID=813;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF087330; AAD04105.1; -;
 DR Interpro: IPR005350; UPF0137.
 DR Pfam: PF03677; UPF0137; 1.
 KW Hypothetical protein; Plasmid.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 46 AA; 5214 MW; D2FDAC41C1960867 CRC64;

Query Match 64.3%; Score 18; DB 2; Length 46;
 Best Local Similarity 40.0%; Pred. No. 12;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
 DB 21 KKNQTAAASLD 30

RESULT 8
 Q8RTC9 PRELIMINARY; PRT; 108 AA.
 ID 08RTC9
 AC 08RTC9;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative portal vertex protein GPO (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CH014;
 RA Pradel N., Leroy-Settin S., Livrelli V.;
 RT "Sequences from Shiga toxin-producing Escherichia coli O91:H21.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF467512; AAL78348.1; -;
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 108 AA; 12028 MW; 350B505A7A03B5B5 CRC64;

Query Match 64.3%; Score 18; DB 2; Length 108;
 Best Local Similarity 40.0%; Pred. No. 25;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
 DB 54 KKASADLDD 63

RESULT 9
 Q9ANS7 PRELIMINARY; PRT; 153 AA.
 ID 09ANS7;
 AC 09ANS7;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE luxT.
 OS Vibrio harveyi.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin Y.H., Miyamoto C.M., Meighen E.A.;
 RT "Cloning and functional studies of a luxO regulator luxT from Vibrio
 RT Blochum. Biophys. Acta 0:0-0(2001).
 DR EMBL: AF321123; AAK09362.1; -;

SO SEQUENCE 153 AA; 17475 MW; 33837BBI2A2A1819B CRC64;
 Query Match 64.3%; Score 18; DB 2; Length 153;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 4; Conservative 0; Mismatches -6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXX 12
 DB 54 KKTDFTAALD 63

RESULT 10
 Q8WV5 PRELIMINARY; PRT; 160 AA.
 AC Q8WV5;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical 17.0 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RA Strusberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019336; AAH19336.1;
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 160 AA; 17041 MW; 967B497AAC065DB8 CRC64;

Query Match 64.3%; Score 18; DB 4; Length 160;
 Best Local Similarity 40.0%; Pred. No. 35;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXX 12
 DB 52 KKSAAESMD 61

RESULT 11
 Q9KL32 PRELIMINARY; PRT; 161 AA.
 AC Q9KL32;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Transcriptional regulator, Tetrahymena.
 GN VCA0917.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406633; PubMed=10952301;
 RA Hodelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
 RA McDonald L., Osterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004419; AAF96814.1;
 DR TIGR; AC09017;
 KW Complete proteome.
 SQ SEQUENCE 161 AA; 18749 MW; AA78003D18984288 CRC64;

Query Match 64.3%; Score 18; DB 16; Length 161;
 Best Local Similarity 40.0%; Pred. No. 35;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXX 12
 DB 62 KKTDFASALD 71

RESULT 12
 O04541 PRELIMINARY; PRT; 171 AA.
 AC O04541;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE F20P5.23 protein.
 GN F20P5.23.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Osborne B.I., Vysotskaya V.S., Toriumi M., Yu G., Oji O., Buehler E.,
 RA Conway A.B., Conway A.R., Dewar K., Feng J., Kim C., Kuritz D., Li Y.,
 RA Shin F., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
 RA Theologis A.;
 RT "The sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1";
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002062; AAB61109.1;
 DR InterPro; IPR003822; PAH.
 DR Pfam; PF02671; PAH; 2.
 SQ SEQUENCE 171 AA; 19992 MW; 691285E59734CA73 CRC64;

Query Match 64.3%; Score 18; DB 10; Length 171;
 Best Local Similarity 40.0%; Pred. No. 37;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXX 12
 DB 16 KKLTTTDAALD 25

RESULT 13
 Q9D854 PRELIMINARY; PRT; 205 AA.
 AC Q9D854;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 1810038D15Rik protein (RIKEN CDNA 1810038D15 gene).
 GN 1810038D15Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gunglrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Yuzhakov Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.,
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK007731; BAB25219.1; -
 DR EMBL: BC003445; AA03445.1; -
 DR MGD: MGI:1916430; 181003BD15Rik.
 DR InterPro: IPR000520; Exonuclease.
 DR Pfam: PF00929; Exonuclease; 1.
 DR SMART: SM00479; EXOIII; 1.
 SQ SEQUENCE 205 AA; 23613 MW; D3FFP9C7014B730E CRC64;
 Query Match 64.3%; Score 18; DB 11; Length 205;
 Best Local Similarity 40.0%; Pred. No. 43;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 KKKXXXXXLD 12
 Db 157 KKAASHRALD 166
 RESULT 14
 Q8X4Z7 PRELIMINARY; PRT; 212 AA.
 AC Q8X4Z7;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Putative tet operon regulator.
 GN YCDC OR 21512 OR ECS1259.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 NCBI_TaxID=83334;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE-21074935; PubMed-11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobleck E.J., Davis N.W., Lam A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.,
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN-O157:H7 / RIMD 0509952;
 RX MEDLINE-21156231; PubMed-11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinozawa H.,
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.",
 RL DNA Res. 8:11-22(2001).
 DR EMBL: AE005301; AAG555629.1; -

DR EMBL: AP002554; BAB34682.1; -
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PF00440; tetr. 1.
 DR PRINTS: PR00455; HHTETR.
 KW Complete proteome.
 SQ SEQUENCE 212 AA; 23703 MW; 5DMA7B85C960FDEC CRC64;
 Query Match 64.3%; Score 18; DB 16; Length 212;
 Best Local Similarity 40.0%; Pred. No. 45;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 KKKXXXXXLD 12
 Db 20 KKAILLSALD 29
 RESULT 15
 Q96609 PRELIMINARY; PRT; 215 AA.
 AC Q96609;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE Surface antigen ariell.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-HM1-IMSS;
 RX MEDLINE-98084495; PubMed-9423879;
 RA Mai Z., Samuelson J.,
 RT "A new gene family (ariel) encodes asparagine-rich Entamoeba
 RT histolytica antigens, which resemble the anebic vaccine candidate
 RT serine-rich E. histolytica protein.",
 RL Infect. Immun. 66:353-355(1998).
 DR EMBL: AF093575; AAC72364.1; -
 SQ SEQUENCE 215 AA; 23641 MW; 00B59B87816A5ECD CRC64;
 Query Match 64.3%; Score 18; DB 5; Length 215;
 Best Local Similarity 40.0%; Pred. No. 45;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 KKKXXXXXLD 12
 Db 50 KKSSNSELD 59
 Search completed: June 5, 2003, 15:55:45
 Job time : 34.9091 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:47:43 ; Search time 40.7273 Seconds
(without alignments)
39.261 Million cell updates/sec

Title: US-09-150-947f-18
Perfect score: 17
Sequence: 1 XXXXXXXXXXXXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /SID2/gcgdata/geneseq/emb1/AA1981.DAT:*
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23: /SID2/gcgdata/geneseq/emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	35.3	2	AA10185	Sequence of synth
2	6	35.3	2	AA37936	Trypsin modulating
3	6	35.3	3	AA40819	Sequence of iragme
4	6	35.3	3	AA04607	Antiviral agent.
5	6	35.3	3	AA00718	Core repeat of cel
6	6	35.3	3	AA25615	Harvey Ras inhibit
7	6	35.3	3	AA36707	Adhesion formation
8	6	35.3	3	AA30728	Igf-mast cell reac
9	6	35.3	3	AA30753	Igf-mast cell reac
10	6	35.3	3	AA53144	RGD peptide deriva

11	6	35.3	3	AA44666	Platelet aggregati
12	6	35.3	3	AA48960	ML4-3 truncated GA
13	6	35.3	3	AA82907	Non-RGD, non-YISGR
14	6	35.3	3	AA70472	Cancer metastasis
15	6	35.3	3	AA64556	RF-1 peptide 1 fro
16	6	35.3	3	AA64722	HPF3 peptide deriv
17	6	35.3	3	AA11094	Platelet-targetin
18	6	35.3	3	AA99823	Active domain from
19	6	35.3	3	AA99825	Mutant chemokine a
20	6	35.3	3	AA99827	Human IL-16 5' end
21	6	35.3	3	AA39130	Platelet-targeting
22	6	35.3	3	AA31143	LDV-peptide capabl
23	6	35.3	3	AA25187	IDA-peptide capabl
24	6	35.3	3	AA25193	RGD-peptide capabl
25	6	35.3	3	AA25173	Angiotensin II pep
26	6	35.3	3	AA64738	Peptide AII(1-3) u
27	6	35.3	3	AA71120	Integrin receptor
28	6	35.3	3	AA48589	Anti-Inflammatory
29	6	35.3	3	AA56245	Anti-Inflammatory
30	6	35.3	3	AA56245	Anti-Inflammatory
31	6	35.3	3	AA56186	Anti-Inflammatory
32	6	35.3	3	AA56197	Anti-Inflammatory
33	6	35.3	3	AA50604	Resin bound cyclic
34	6	35.3	3	AA50605	Resin bound cyclic
35	6	35.3	3	AA43494	Linker for dual av
36	6	35.3	3	AA39889	Asparaginyl endope
37	6	35.3	3	AA30593	Amino acid sequenc
38	6	35.3	3	AA30593	Amino acid sequenc
39	6	35.3	3	AA32860	Fibronectin protei
40	6	35.3	3	AA32860	Fibronectin protei
41	6	35.3	3	AA32860	Fibronectin protei
42	6	35.3	3	AA32860	Fibronectin protei
43	6	35.3	3	AA32860	Fibronectin protei
44	6	35.3	3	AA32860	Fibronectin protei
45	6	35.3	3	AA32860	Fibronectin protei

ALIGNMENTS

RESULT 1	AA10185	AA10185 standard; Protein; 2 AA.
ID	AA10185	AA10185 standard; Protein; 2 AA.
XX	AA10185	AA10185 standard; Protein; 2 AA.
AC	AA10185	AA10185 standard; Protein; 2 AA.
XX	AA10185	AA10185 standard; Protein; 2 AA.
DT	16-AUG-2002 (updated)	16-AUG-2002 (updated)
DT	14-AUG-1992 (first entry)	14-AUG-1992 (first entry)
DE	Sequence of synthetic polypeptide for the prodn. of aspartame.	Sequence of synthetic polypeptide for the prodn. of aspartame.
XX	Aspartyl-phenylalanine methyl ester; artificial sweetener;	Aspartyl-phenylalanine methyl ester; artificial sweetener;
KW	aspartame.	aspartame.
XX	Synthetic.	Synthetic.
OS	EP36258-A.	EP36258-A.
PN	23-SEP-1981.	23-SEP-1981.
XX	02-MAR-1981; 81EP-0300857.	02-MAR-1981; 81EP-0300857.
PF	14-MAR-1980; 80US-0130462.	14-MAR-1980; 80US-0130462.
PR	(CETU-) CETUS CORP.	(CETU-) CETUS CORP.
XX	Rose JE, White TJ, Bahl CP;	Rose JE, White TJ, Bahl CP;
PI	WPI; 1981-72133D/40.	WPI; 1981-72133D/40.
XX	N-PSDB; AA10059.	N-PSDB; AA10059.
DR	Aspartame prodn. from synthetic polypeptide - produced by cloned	Aspartame prodn. from synthetic polypeptide - produced by cloned
XX	microorganism	microorganism
PT		

XX Disclosure; page 5; 18bp; English.
 XX
 CC The inventors claim a method for the prodn. of aspartame by first
 CC synthesizing double-stranded DNA in which a coding strand has
 CC alternating codons for Asp and the Phe in sufficient number to
 CC produce a polypeptide which is stable in predetermined host
 CC microorganisms. The DNA strand is then inserted into a cloning
 CC vehicle so that the resulting chimera directs the synthesis of the
 CC Asp-Phe protein. This protein is then cleaved with CNBr or trypsin
 CC to release the peptide which, after benzylation, can be fragmented
 CC by digestion with chymotrypsin.
 CC (Updated on 16-AUG-2002 to add missing OS field.)
 CC
 SQ Sequence 2 AA;
 Query Match 35.3%; Score 6; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 DB 1 D 1
 RESULT 2
 AAB37936
 ID AAB37936 standard; peptide; 2 AA.
 XX
 AC AAB37936;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Trypsin modulating oostatic factor (TMOF) peptide SEQ ID 41.
 XX
 KW Trypsin modulating oostatic factor; TMOF; pesticide; pest control;
 KW digestive enzyme synthesis inhibition; mosquito larvae; coleopteran;
 KW lepidopteran; dipteran; blood-sucking insect; Diptera; Nematocera;
 KW Colicidae; Culicidae; Corethrinae; Ceratopogonidae; Simuliidae.
 XX
 OS Synthetic.
 XX
 PN WO200063233-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 18-APR-2000; 2000WO-US10235.
 XX
 PR 21-APR-1999; 99US-0295996.
 XX
 PA (UNFL) UNIV FLORIDA RES FOUND INC.
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Borovsky D, Linderman RJ;
 XX
 DR WPI; 2000-687156/67.
 XX
 PT Novel trypsin modulating oostatic factor compound peptides, useful for
 PT pest control including pests of agricultural crops -
 XX
 PS Claim 3; Page 33; 50pp; English.
 XX
 CC This invention relates to a trypsin modulating oostatic factor (TMOF)
 CC compound. The compound specifically does not include the TMOF analogue
 CC peptides represented by AAB37942 - AAB37949. Sequences AAB37900 -
 CC AAB37941 are TMOF analogues which may be included in the composition. The
 CC TMOF compound has pesticidal activity and is an inhibitor of pest
 CC digestive enzyme synthesis. The TMOF compound is useful for controlling
 CC pests such as mosquito larvae, coleopterans, lepidopterans, dipterans or
 CC blood-sucking insects of order Diptera, suborder Nematocera, family
 CC Colicidae or subfamily Culicinae, Corethrinae, Ceratopogonidae and
 CC Simuliidae.

SQ Sequence 2 AA;
 Query Match 35.3%; Score 6; DB 21; Length 2;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 DB 2 D 2
 RESULT 3
 AAP40819
 ID AAP40819 standard; peptide; 3 AA.
 XX
 AC AAP40819;
 XX
 DT 03-AUG-1992 (first entry)
 XX
 DE Sequence of fragment D, corresp. to residues 25-27 of human
 DE pancreatic growth hormone releasing factor (somatostatin) (hpgRF).
 XX
 KW Hormone; dwarfism; therapy; retarded growth;
 KW anabolic protein deficiency; growth promoter; lactation.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Modified-site 1 Location/Qualifiers
 FT 1 /Label= Boc-D(OBzl)
 FT /note= "Boc-tertbutyloxycarbonyl (carbamate);
 FT OBzl=ester benzyllique"
 FT Modified-site 3 /Label= M-NH-NH2
 FT
 XX
 PN AU8424774-A.
 XX
 PD 30-AUG-1984.
 XX
 PF 20-FEB-1984; 84AU-0400343.
 XX
 PR 29-NOV-1983; 83FR-0019058.
 PR 21-FEB-1983; 83FR-0002781.
 XX
 PA (SNFI) SANOFI SA.
 XX
 PI Diaz J, Demarne H, Roncucci R, Schmelck PH;
 XX
 DR WPI; 1984-256760/42.
 XX
 PT Synthesis of hpgRF in liquid phase reactions - with use of new
 PT peptide fragments
 XX
 PS Claim 4; Page 67; 76pp; French.
 XX
 CC The inventors claim hpgRF fragments used for the synthesis of hpgRF.
 CC Using the method somatostatin can be obt'd. on a large scale with
 CC good yield and good purity. The prod. is used in man for the
 CC treatment of dwarfism and retarded growth and for anabolic protein
 CC deficiencies. In animals it is useful for promoting wt. growth for
 CC increased prodn. lactation etc. This index is based on Ep-122818,
 CC which is the equivalent of AU8424774.
 CC
 SQ Sequence 3 AA;
 Query Match 35.3%; Score 6; DB 5; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 DB 1 D 1

```

RESULT 5
AAR04607
ID AAR04607 standard; peptide; 3 AA.
XX
AC AAR04607;
XX
DT 05-SEP-1990 (first entry)
XX
DE Antiviral agent.
XX
KM Antiviral; M2; poliovirus; polio; hepatitis.
XX
OS Synthetic.
XX
PN JP02078631-A.
XX
PD 19-MAR-1990.
XX
PF 14-SEP-1988; 88JP-0228843.
XX
PR 14-SEP-1988; 88JP-0228843.
XX
PA (NIHA ) NIPPON MINING KK.
XX
DR WPI; 1990-129060/17.
XX
PT Antiviral agent contg. tripeptide (unit) -
PT of basic aminoacid, then alanine, glycine or sarcosine, and
PT acidic aminoacid, effective against virus with protein-terminated DNA
PT or RNA.
XX
PS
XX
SS Disclosure; 4pp; Japanese.
XX
CC Peptide is effective against inhibiting propagation of DNA or RNA
CC bonded, protein containing viruses eg. Poliovirus, Hepatitis virus.
XX
SQ Sequence 3 AA;

Query Match 35.3%; Score 6; DB 11; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 12 D-12
|
DB 3 D 3

RESULT 5
AAR00718
ID AAR00718 standard; peptide; 3 AA.
XX
AC AAR00718;
XX
DT 29-MAY-1990 (first entry)
XX
DE Core repeat of cell-adhesive protein.
XX
KM Cell adhesion; anti-metastatic agent; immunomodulation; core repeat.
XX
PN EP347931-A.
XX
PD 27-DEC-1989.
XX
PF 23-JUN-1989; 89EP-0111468.
XX
PR 24-JUN-1988; 88JP-0156133.
XX
PA (AZUMA/) AZUMA I.
XX
PT Sakai I, Nishi N, Azuma I, Tokura S;
XX
WPI; 1990-001305/01.
DR

```

Polypeptide with repeated sequences of cell adhesion protein used as anti-metastatic agent for cancer and agonist or antagonist of cell-adhesion proteins

Claim 2; page 14; 16pp; English.

Peptide core is repeated 2-20 times to form a cell-adhesive protein of mol. wt. 1,500-5,000. The protein is an (ant)agonist of cell-adhesive proteins such as fibronectin. It has high antimetastatic activity against cancer and can be used in immunomodulation, wound healing, platelet aggregation inhibition and alleviation of neuro-disorders. See also AAR00722.

Sequence 3 AA:

Query Match 35.3%; Score 6; DB 11; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 D 12
1
3 D 3

RESULT 6
AAR25615
AAR25615 standard; peptide; 3 AA.
AAR25615;
20-JAN-1993 (first entry)
Harvey Ras Inhibitor - Ras 30-32.
GTPase; activating protein; GAP; oncogenesis; cancer; truncated; colorectal; exocrine pancreatic; myeloid leukaemia; adenyl acylase.
Synthetic.
EP496162-A.
29-JUL-1992.
16-DEC-1991; 91EP-0311658.
24-DEC-1990; 90US-0632891.
(MERI) MERCK & CO INC.
Freidinger RM, Garaky VM, Gibbs JB, Schaber MD, Sigal IS;
WPI. 1992-251427/31.
Synthetic peptide inhibitors of Ras-GAP interaction - as antitumour agents against e.g. colorectal carcinoma, exocrine pancreatic carcinoma and myeloid leukaemia

Claim 3; Page 7; 31pp; English.

The peptide corresponds to a C- and N-terminal truncated version of the prod. of the Harvey ras oncogene from residues 17-44, i.e. from residues 30-32. The peptide is capable of binding to GRPase activating protein (GAP) thus inhibiting Ras activation by GAP and inhibiting Ras-dependent cell transformation. Derivs. of the Ras peptide are also provided, comprising C-terminal truncations, N-terminal truncations, or modifications of specific amino acids, e.g. the most potent Ras inhibitor is Ras 17-32. Oncogenic forms of Ras occur in various human cancers, e.g. colorectal carcinoma, exocrine pancreatic carcinoma and myeloid leukaemias. Ras complexed with GTP can bind GAP and this is thought to be the important step in the transformation activity of Ras. The peptide is also capable of inhibiting GAP as well as the interaction of Ras with yeast

CC adenylyl acylase. See also AAR25602-29.
XX
SQ Sequence 3 AA;

Query Match
Best Local Similarity 35.3%; Score 6; DB 13; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 7
AAR36707
ID AAR36707 standard; peptide; 3 AA.

AC AAR36707;

DT 26-MAY-1993 (first entry)

DE Adhesion formation prevention RGD-contg. peptide.

KW Tissue repair; peritoneum; surgery; post-surgically; inhibition;
platelet aggregation; cardiovascular; orthopedic; thoracic;
ophthalmic; CNS; use.

OS Synthetic.

PN MO9308818-A.

PD 13-MAY-1993.

PF 06-NOV-1992; 92WO-US0494.

PR 07-NOV-1991; 91US-0789231.

PA (UTSC-) UNIV SOUTHERN CALIFORNIA.

PI Dizerega GS, Rodgers KE;

DR WPI, 1993-167381/20.

PT Prevention of adhesion formation, partic. post-surgically - comprises
administering a RGD-contg. peptide for a time sufficient to permit
tissue repair

PS Example: Page 18; 22pp; English.

CC The sequence is that of an RGD-contg. peptide which is used in a
method for prevention of adhesion formation for a time sufficient
to permit tissue repair. The method is used for minimizing or
preventing adhesion formation, partic. in the peritoneum following
surgery, but also for e.g. cardiovascular, orthopedic, thoracic,
ophthalmic, CNS and other uses. In addn., the peptide inhibits
platelet aggregation and does not induce inflammation or trauma
at the site of administration.

CC
SQ Sequence 3 AA;

Query Match
Best Local Similarity 35.3%; Score 6; DB 14; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 3 D 3

RESULT 8
AAR30728
ID AAR30728 standard; peptide; 3 AA.
XX

AC AAR30728;
XX
XX 20-MAY-1993 (first entry)
DT
XX

DE IGE-mast cell reaction preventing peptide intermediate.

KW Basophil; protective group; fragment condensing.

XX
XX Synthetic.

OS
FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-t-butoxycarbonyl-beta-benzyl-L-aspartyl"

PN JP04360898-A.

PD 14-DEC-1992.

PF 04-JUN-1991; 91JP-0159394.

PR 04-JUN-1991; 91JP-0159394.

PA (TANA) TANABE SEIYAKU CO.

DR WPI, 1993-032710/04.

XX L-Aspartyl-L-seryl-L-aspartyl-L-prolyl-L-arginine prepn.

PT Involves fragment-condensing tripeptide with amino-protected
di-peptide to form penta-peptide

PS Claim 7; Page 2; 8pp; Japanese.

CC The prepn. of DSPR is claimed and involves e.g. fragment-condensing
C-protected tripeptide with N-protected dipeptide to form pentapeptide
and then removing the protective gps.
CC N-t-butoxycarbonyl-beta-benzyl-L-aspartyl-L-prolyl-L-arginine is a
new cpd."

SQ Sequence 3 AA;

Query Match
Best Local Similarity 35.3%; Score 6; DB 14; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 9

AAR30753
ID AAR30753 standard; peptide; 3 AA.

AC AAR30753;

DT 26-MAY-1993 (first entry)

DE IGE-mast cell reaction inhibitory peptide prepn. peptide.

XX Physiologically active; basophil; tripeptide.

XX Synthetic.

OS Key Location/Qualifiers

FH Modified-site 1 /note= "N-t-butoxycarbonyl-beta-benzyl-L-Asp"

FT Modified-site 5 /note= "N(G)-nitro-L-Arg benzyl ester"

PN JP04360899-A.

PD 14-DEC-1992.

AC AAR48960;
 XX
 DT 12-SEP-1994 (first entry)
 XX
 DE NL4-3 truncated GAG C-terminal peptide.
 XX
 KM HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
 KM naturally occurring virus; NOV; translation; replication; infectivity;
 KM hepatitis B; HIV-2; SIV; flip-over PCR.
 XX
 OS Synthetic.
 XX
 PN WO9403596-A.
 XX
 PD 17-FEB-1994.
 XX
 PF 30-JUL-1993; 93WO-US071179.
 XX
 PR 30-JUL-1992; 92US-0921104.
 XX
 PA (UYHA-) UNIV HAMAM.
 XX
 PI Hu W, Wang J;
 XX
 DR MPI: 1994-065685/08.
 DR N-PSDB: AAO57688.
 XX
 PT New antisense viruses and anti-sense-ribozyme viruses - used for
 PT treating or preventing viral infections, partic. HIV-1, HIV-2 or
 PT SIV infection
 XX
 PS Disclosure: Page 108; 167pp; English.
 XX
 CC This sequence is encoded by a PCR fragment of NL4-3 and represents the
 CC C-terminal peptide fragment of the truncated GAG protein. The DNA
 CC encoding this fragment was ligated into ClaI/SalI digested px and the
 CC corresponding plasmid was used to produce the antisense virus of the
 CC invention. Antisense or truncated RNAs expressed by these viruses
 CC bind to the mRNAs expressed by the naturally occurring viruses (NOVs)
 CC and prevent the NOV from being translated into proteins, thereby
 CC preventing the NOV from replicating. The antisense viruses maintain
 CC the infectivity of the NOV, allowing antisense RNAs to reach the
 CC mRNAs of the natural viruses. Antisense viruses such as these may be
 CC used for treating or preventing a viral infection, particularly HIV-1,
 CC HIV-2 or SIV infection or hepatitis B infection.
 CC
 SQ Sequence 3 AA;
 Query Match 35.3%; Score 6; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 2 D 2
 RESULT 13
 AAR82907
 ID AAR82907 standard; peptide; 3 AA.
 XX
 AC AAR82907;
 XX
 DT 20-DEC-1995 (first entry)
 XX
 DE Non-RGD, non-YISGR cancer metastasis inhibitory peptide #1.
 XX
 KM Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;
 KM water soluble polysaccharide; metastasis; wound; immunogenicity.
 XX
 OS Synthetic.
 XX
 PN JP07089999-A.

XX
 PD 04-APR-1995.
 XX
 PF 17-SEP-1993; 93JP-0254779.
 XX
 PR 17-SEP-1993; 93JP-0254779.
 XX
 PA (JAPG) NIPPON ZEON KK.
 XX
 DR MPI: 1995-167254/22.
 XX
 PT Cancer metastasis inhibitive peptide derivs. - useful for inhibition
 PT of cancer metastasis, healing of wounds and regulation of
 PT immunogenicity.
 XX
 PS Disclosure: Page 3; 6pp; Japanese.
 XX
 CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
 CC inhibit cancer metastasis. They are composed of an adhesive peptide
 CC with a core sequence selected from: RGD (AAR70472-85), YIGSR
 CC (AAR70486-90) or other sequence (AAR82907-24), linked to a water soluble
 CC polysaccharide, preferably a water soluble dextran, at the C-terminus.
 CC The peptides are useful in inhibiting cancer metastasis, healing wounds
 CC and the regulation of immunogenicity.
 CC
 SQ Sequence 3 AA;
 Query Match 35.3%; Score 6; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 2 D 2
 RESULT 14
 AAR70472
 ID AAR70472 standard; peptide; 3 AA.
 XX
 AC AAR70472;
 XX
 DT 20-DEC-1995 (first entry)
 XX
 DE Cancer metastasis inhibitory peptide core RGD sequence.
 XX
 KM Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;
 KM water soluble polysaccharide; metastasis; wound; immunogenicity.
 XX
 OS Synthetic.
 XX
 PN JP07089999-A.
 XX
 PD 04-APR-1995.
 XX
 PF 17-SEP-1993; 93JP-0254779.
 XX
 PR 17-SEP-1993; 93JP-0254779.
 XX
 PA (JAPG) NIPPON ZEON KK.
 XX
 DR MPI: 1995-167254/22.
 XX
 PT Cancer metastasis inhibitive peptide derivs. - useful for inhibition
 PT of cancer metastasis, healing of wounds and regulation of
 PT immunogenicity.
 XX
 PS Disclosure: Page 2; 6pp; Japanese.
 XX
 CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
 CC inhibit cancer metastasis. They are composed of an adhesive peptide
 CC with a core sequence selected from: RGD (AAR70472-85), YIGSR
 CC (AAR70486-90) or other sequence (AAR82907-24), linked to a water soluble
 CC polysaccharide, preferably a water soluble dextran, at the C-terminus.
 CC The peptides are useful in inhibiting cancer metastasis, healing wounds
 CC and the regulation of immunogenicity.

CC polypeptide, preferably a water soluble dextran, at the C-terminus.
 CC The peptides are useful in inhibiting cancer metastasis, healing wounds
 CC and the regulation of immunogenicity.

XX Sequence 3 AA;

Query Match 35.3%; Score 6; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12

Db 3 D 3

RESULT 15

ID AAR64556 standard; Peptide; 3 AA.

AC AAR64556;

DT 01-SEP-1995 (first entry)

DE RF-1 peptide 1 from respiratory syncytial virus.

KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 human immunodeficiency virus; transmembrane protein; gp41;

KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;
 RSV.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note- "optionally has an amino, acetyl,
 9-fluorenylmethoxy-carbonyl, hydrophobic or
 macromolecular carrier gp. attached"

FT Modified-site 3 /note- "optionally has a carboxyl, amide, hydrophobic
 or macromolecular carrier gp. attached"

FT Modified-site 3 /note- "optionally has a carboxyl, amide, hydrophobic
 or macromolecular carrier gp. attached"

XX WO9428920-A.

XX 22-DEC-1994.

PF 07-JUN-1994; 94NO-US05739.

PR 07-JUN-1993; 93US-0073028.

XX (UYDG-) UNIV DUKE.

PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 Petteway SR, Wild CT;

DR MPI; 1995-036105/05.

PT Computer search generated synthetic peptides - are inhibitors of
 HIV transmission

XX Claim 14; Page 137; 182pp; English.

CC AAR64556-589 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncytial virus (RSV) (AAR64590) which have been
 CC truncated at the carboxy terminus. The peptides are DP-178 like
 CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
 CC isolate LAI transmembrane protein gp41. It forms a putative alpha
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a
 CC leucine zipper motif. The peptides complex via non-covalent
 CC protein-protein interactions. The peptide derivatives were
 CC identified by a computer assisted peptide sequence search. The
 CC antiviral activity of this peptide is not stated in the
 CC specification.

XX Sequence 3 AA;

Query Match 35.3%; Score 6; DB 16; Length 3;
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12

Db 3 D 3

Search completed: June 5, 2003, 16:00:25
 Job time : 40.7273 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw.model

Run on: June 5, 2003, 15:23:33 ; Search time 10.5455 Seconds
(without alignments)
33.481 Million cell updates/sec

Title: US-09-150-947F-18
Perfect score: 17
Sequence: 1 xxxxxxxxxxxx 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	35.3	2	1	US-07-820-154A-15
2	6	35.3	2	1	US-07-820-154A-23
3	6	35.3	2	1	US-07-820-154A-33
4	6	35.3	2	1	US-07-820-154A-39
5	6	35.3	2	1	US-08-358-160-171
6	6	35.3	2	1	US-08-153-799-20
7	6	35.3	2	2	US-08-097-554A-15
8	6	35.3	2	2	US-08-097-554A-23
9	6	35.3	2	2	US-08-097-554A-33
10	6	35.3	2	2	US-08-097-554A-39
11	6	35.3	2	2	US-08-539-432-15
12	6	35.3	2	2	US-08-539-432-16
13	6	35.3	2	2	US-08-539-432-17
14	6	35.3	2	3	US-09-327-424-2
15	6	35.3	2	3	US-08-480-640A-15
16	6	35.3	2	3	US-08-480-640A-23
17	6	35.3	2	3	US-08-480-640A-33
18	6	35.3	2	3	US-08-480-640A-39
19	6	35.3	2	3	US-08-295-802-15
20	6	35.3	2	3	US-08-295-802-23
21	6	35.3	2	3	US-08-295-802-33
22	6	35.3	2	3	US-08-295-802-39
23	6	35.3	2	4	US-09-326-335-2
24	6	35.3	2	4	US-08-488-237A-15
25	6	35.3	2	4	US-08-488-237A-23
26	6	35.3	2	4	US-08-488-237A-33
27	6	35.3	2	4	US-08-488-237A-39

28	6	35.3	2	4	US-08-375-992A-15	Sequence 15, App1
29	6	35.3	2	4	US-08-375-992A-23	Sequence 23, App1
30	6	35.3	2	4	US-08-375-992A-33	Sequence 33, App1
31	6	35.3	2	4	US-08-375-992A-39	Sequence 39, App1
32	6	35.3	2	4	US-09-295-996B-23	Sequence 23, App1
33	6	35.3	2	4	US-09-295-996B-35	Sequence 35, App1
34	6	35.3	2	4	US-09-295-996B-58	Sequence 58, App1
35	6	35.3	2	5	PCT-US93-00324-15	Sequence 15, App1
36	6	35.3	2	5	PCT-US93-00324-23	Sequence 23, App1
37	6	35.3	2	5	PCT-US93-00324-33	Sequence 33, App1
38	6	35.3	2	5	PCT-US93-00324-39	Sequence 39, App1
39	6	35.3	3	1	US-07-748-943-2	Sequence 2, App1
40	6	35.3	3	1	US-07-748-943-1	Sequence 1, App1
41	6	35.3	3	1	US-08-169-524-6	Sequence 6, App1
42	6	35.3	3	1	US-08-081-539-117	Sequence 117, App
43	6	35.3	3	1	US-08-251-027-1	Sequence 1, App1
44	6	35.3	3	1	US-08-251-027-2	Sequence 2, App1
45	6	35.3	3	1	US-08-251-027-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-07-820-154A-15
Sequence 15, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-15
Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 D 1
RESULT 2
US-07-820-154A-23

Sequence 23, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-23

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 3
US-07-820-154A-33
Sequence 33, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-33

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 4
US-07-820-154A-39
Sequence 39, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-820-154A-39

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 5
US-08-358-160-171
Sequence 171, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LET, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-SEP-1988
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-171

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 D 12
1 D 1

RESULT 6
US-08-153-799-20
Sequence 20, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J

APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-799-20

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 D 12
1 D 1

RESULT 7
US-08-097-554A-15
Sequence 15, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-15

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
1 D 1

RESULT 8
US-08-097-554A-23
Sequence 23, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-23

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
1 D 1

RESULT 9
US-08-097-554A-33
Sequence 33, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-554A-33

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
1 D 1

RESULT 10
US-08-097-554A-39
Sequence 39, Application US/08097554A
Patent No. 5869312
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: JULY 22, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-534A-39

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 11
US-08-539-432-15
Sequence 15, Application US/08539432
Patent No. 5872210
GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: TRANSFRAME INHIBITORY
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: linear
US-08-539-432-15

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 12
US-08-539-432-16
Sequence 16, Application US/08539432
Patent No. 5872210
GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: TRANSFRAME INHIBITORY
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: linear
US-08-539-432-16

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 13
US-08-539-432-17
Sequence 17, Application US/08539432
Patent No. 5872210
GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: TRANSFRAME INHIBITORY
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10054

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,432
FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
US-08-539-432-17

Query Match 35.3%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 14
US-09-327-424-2
Sequence 2, Application US/09327424
Patent No. 6027903
GENERAL INFORMATION:
APPLICANT: Eyre, David R
TITLE OF INVENTION: KIT FOR DETECTING ANALYTE INDICATIVE OF TYPE I COLLAGEN
TITLE OF INVENTION: RESORPTION IN VIVO (as amended)
FILE REFERENCE: WROS-1-14019
CURRENT APPLICATION NUMBER: US/09/327,424
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2
TYPE: PPT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: N-telopeptide sequence of type II collagen
US-09-327-424-2

Query Match 35.3%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 15
US-08-480-640A-15
Sequence 15, Application US/08480640A
Patent No. 6033904
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-640A-15

Query Match 35.3%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

Search completed: June 5, 2003, 15:32:44
Job time : 10.5455 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:01 ; Search time 14.5455 Seconds
(without alignments)
85.173 Million cell updates/sec

Title: US-09-150-947f-18
Perfect score: 17
Sequence: 1 xxxxxxxxxxxd 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

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11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	35.3	2	9	US-10-187-339-6
2	6	35.3	2	9	US-10-206-699-296
3	6	35.3	2	10	US-09-982-172-8
4	6	35.3	2	10	US-09-982-172-105
5	6	35.3	3	9	US-09-900-936-11
6	6	35.3	3	9	US-09-840-277-31
7	6	35.3	3	9	US-09-747-408-21
8	6	35.3	3	9	US-10-014-162-37
9	6	35.3	3	9	US-10-039-876A-3
10	6	35.3	3	9	US-10-039-876A-4
11	6	35.3	3	9	US-10-015-879-58
12	6	35.3	3	9	US-10-226-956-316
13	6	35.3	3	9	US-10-226-956-317
14	6	35.3	3	9	US-10-226-956-318
15	6	35.3	3	9	US-10-226-956-319
16	6	35.3	3	9	US-10-128-198-1
17	6	35.3	3	9	US-10-237-850-81
18	6	35.3	3	9	US-10-032-818-6
19	6	35.3	3	9	US-10-281-652-11

20	6	35.3	3	9	US-10-283-838-13	Sequence 13, Appl
21	6	35.3	3	9	US-10-163-587A-19	Sequence 19, Appl
22	6	35.3	3	9	US-10-141-531-15	Sequence 15, Appl
23	6	35.3	3	9	US-10-141-531-16	Sequence 16, Appl
24	6	35.3	3	9	US-10-141-531-17	Sequence 17, Appl
25	6	35.3	3	9	US-10-141-531-18	Sequence 18, Appl
26	6	35.3	3	9	US-10-141-531-19	Sequence 19, Appl
27	6	35.3	3	9	US-10-141-531-20	Sequence 20, Appl
28	6	35.3	3	10	US-09-866-824A-9	Sequence 13, App
29	6	35.3	3	10	US-09-792-200B-19	Sequence 19, Appl
30	6	35.3	3	10	US-09-771-192-11	Sequence 11, Appl
31	6	35.3	3	10	US-09-853-918-1	Sequence 1, Appl
32	6	35.3	3	10	US-09-853-918-6	Sequence 6, Appl
33	6	35.3	3	10	US-09-853-918-14	Sequence 14, Appl
34	6	35.3	3	10	US-09-867-847-30	Sequence 30, Appl
35	6	35.3	3	10	US-09-822-261-7	Sequence 7, Appl
36	6	35.3	3	10	US-09-312-762A-12	Sequence 12, Appl
37	6	35.3	3	10	US-09-982-172-184	Sequence 184, App
38	6	35.3	3	10	US-09-837-697A-11	Sequence 11, Appl
39	6	35.3	3	12	US-10-003-674A-6	Sequence 6, Appl
40	6	35.3	4	1	US-08-464-363-35	Sequence 35, Appl
41	6	35.3	4	1	US-08-610-220A-2	Sequence 2, Appl
42	6	35.3	4	1	US-08-610-220A-7	Sequence 7, Appl
43	6	35.3	4	1	US-08-610-220A-8	Sequence 8, Appl
44	6	35.3	4	1	US-08-610-220A-8	Sequence 8, Appl
45	6	35.3	4	8	US-08-765-244-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-10-187-339-6
Sequence 6, Application US/10187339
Publication No. US20030084478A1
GENERAL INFORMATION:
APPLICANT: Ream, Walt et al.,
TITLE OF INVENTION: Plants Having Enhanced Call Resistance and
TITLE OF INVENTION: Methods and Compositions for Producing the Same
FILE REFERENCE: 53629
CURRENT APPLICATION NUMBER: US/10/187,339
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/434,837
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,185
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-187-339-6

Query Match 35.3%: Score 6; DB 9; Length 2;
Best Local Similarity 100.0%: Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

OY 12 D 12
Db 2 D 2

RESULT 2
US-10-206-699-296
Sequence 296, Application US/10206699
Publication No. US20030100510A1
GENERAL INFORMATION:
APPLICANT: Sundaramoorthy, M.
TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
FILE REFERENCE: MHB 01-1017
CURRENT APPLICATION NUMBER: US/10/206,699

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;; CURRENT FILING DATE: 2002-07-26
;; PRIOR APPLICATION NUMBER: US 60/308,523
;; PRIOR FILING DATE: 2001-07-27
;; PRIOR APPLICATION NUMBER: US 60/351,289
;; PRIOR FILING DATE: 2001-10-29
;; PRIOR APPLICATION NUMBER: US 60/366,854
;; PRIOR FILING DATE: 2002-03-22
;; PRIOR APPLICATION NUMBER: US 60/385,362
;; PRIOR FILING DATE: 2002-06-03
;; NUMBER OF SEQ ID NOS: 307
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 296
;; LENGTH: 2
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-206-699-296

Query Match
Best Local Similarity 35.3%; Score 6; DB 9; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 3
US-09-982-172-8
;; Sequence 8, Application US/099822172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Emil Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
;; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 8
;; LENGTH: 2
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-8

Query Match
Best Local Similarity 35.3%; Score 6; DB 10; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 4
US-09-982-172-105
;; Sequence 105, Application US/09982172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Emil Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
;; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 105
;; LENGTH: 2
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;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-105

Query Match
Best Local Similarity 35.3%; Score 6; DB 10; Length 2;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 5
US-09-900-936-11
;; Sequence 11, Application US/09900936
;; Patent No. US20020165141A1
;; GENERAL INFORMATION:
;; APPLICANT: Rodgers, Kathleen
;; APPLICANT: dizegga, Gere
;; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
;; FILE REFERENCE: 00-506-A
;; CURRENT APPLICATION NUMBER: US/09/900,936
;; CURRENT FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 11
;; LENGTH: 3
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: AII (1-3)
US-09-900-936-11

Query Match
Best Local Similarity 35.3%; Score 6; DB 9; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 6
US-09-840-277-31
;; Sequence 31, Application US/09840277
;; Patent No. US20020168363A1
;; GENERAL INFORMATION:
;; APPLICANT: FEIGE, ULRICH
;; APPLICANT: KOHNO, TADAHITO
;; APPLICANT: LACEY, DAVID LEE
;; APPLICANT: BOONE, THOMAS CHARLES
;; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;; FILE REFERENCE: A-688A
;; CURRENT APPLICATION NUMBER: US/09/840,277
;; CURRENT FILING DATE: 2001-08-14
;; PRIOR APPLICATION NUMBER: 60/198,919
;; PRIOR FILING DATE: 2000-04-21
;; PRIOR APPLICATION NUMBER: 60/201,394
;; PRIOR FILING DATE: 2000-05-03
;; NUMBER OF SEQ ID NOS: 135
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 31
;; LENGTH: 3
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-31
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Query Match 35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 3 D 3

RESULT 7

US-09-747-408-21
; Sequence 21, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-21

Query Match 35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 8

US-10-014-162-37
; Sequence 37, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-014-162-37

Query Match 35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 9

US-10-039-876A-3
; Sequence 3, Application US/10039876A
; Publication No. US20030032792A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Blumberg, Hal
; TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, 2219A
; FILE REFERENCE: 97-63C1
; CURRENT APPLICATION NUMBER: US/10/039,876A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/061,712
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: US 09/167,513
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif 1, corresponding to residues 127 to 129 of
; OTHER INFORMATION: SEQ ID NO:2
US-10-039-876A-3

Query Match 35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 10

US-10-039-876A-4
; Sequence 4, Application US/10039876A
; Publication No. US20030032792A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Blumberg, Hal
; TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, 2219A
; FILE REFERENCE: 97-63C1
; CURRENT APPLICATION NUMBER: US/10/039,876A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/061,712
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: US 09/167,513
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif 2, corresponding to residues 156 to 158 of
; OTHER INFORMATION: SEQ ID NO:2
US-10-039-876A-4

Query Match 35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 11

US-10-015-979-58
; Sequence 58, Application US/10015979
; Publication No. US20030036050A1

```
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; APPLICANT: Verhaert, Raymond M.D.
; APPLICANT: Beekwilder, Martinus J.
; APPLICANT: Aehle, Wolfgang
; TITLE OF INVENTION: Enzyme Selection
; FILE REFERENCE: 2183-520705
; CURRENT APPLICATION NUMBER: US/10/015,979
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCF/NL00/00399
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/138,443
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CB4 domain of mutant 13
; NAME/KEY: SITE
; LOCATION: (1)..(3)
; OTHER INFORMATION:
; US-10-015-979-58
```

```
Query Match          35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      12 D 12
DB      3 D 3
```

```
RESULT 12
US-10-226-956-316
; Sequence 316, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padminti
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 316
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-10-226-956-316
```

```
Query Match          35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      12 D 12
DB      1 D 1
```

```
RESULT 13
US-10-226-956-317
```

```
; Sequence 317, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padminti
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 317
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-10-226-956-317
```

```
Query Match          35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      12 D 12
DB      1 D 1
```

```
RESULT 14
US-10-226-956-318
; Sequence 318, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padminti
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 318
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-10-226-956-318
```

```
Query Match          35.3%; Score 6; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      12 D 12
DB      1 D 1
```

```
RESULT 15
US-10-226-956-319
; Sequence 319, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
```

; APPLICANT: Brophy, Colleen
 ; APPLICANT: Komalavilas, Padmini
 ; APPLICANT: Panilch, Alyssa
 ; APPLICANT: Joshi, Lokesh
 ; APPLICANT: Seal, Brandon L.
 ; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
 ; FILE REFERENCE: ASU-1061-US
 ; CURRENT APPLICATION NUMBER: US/10/226,956
 ; CURRENT FILING DATE: 2002-08-23
 ; PRIOR APPLICATION NUMBER: 60/314,535
 ; PRIOR FILING DATE: 2001-08-23
 ; NUMBER OF SEQ ID NOS: 320
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 319
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-10-226-956-319

Query Match 35.3%; Score 6; DB 9; Length 3;
 Best Local Similarity 100.0%; Pred. No. 3.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 1 D 1

Search completed: June 5, 2003, 15:49:05
 Job time : 14.5455 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:24:01 ; Search time 11.8182 seconds
(without alignments)
97.613 Million cell updates/sec

Title: US-09-150-947f-18
Perfect score: 17
Sequence: 1 XXXXXXXXXXXXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	35.3	4	2	140697
2	6	35.3	4	2	A41890
3	6	35.3	4	2	D41654
4	6	35.3	4	2	A32480
5	6	35.3	4	2	I51049
6	6	35.3	4	2	PT0271
7	6	35.3	4	2	B53284
8	6	35.3	4	2	PT0696
9	6	35.3	4	2	PT0711
10	6	35.3	4	2	A26209
11	6	35.3	4	2	A32516
12	6	35.3	5	2	C23751
13	6	35.3	5	2	A26830
14	6	35.3	5	2	A32014
15	6	35.3	5	2	B31836
16	6	35.3	5	2	B60274
17	6	35.3	5	2	D60274
18	6	35.3	5	2	S70615
19	6	35.3	5	2	P00689
20	6	35.3	5	2	PT0267
21	6	35.3	5	2	PT0281
22	6	35.3	5	2	PT0308
23	6	35.3	5	2	PT0596
24	6	35.3	5	2	PT0513
25	6	35.3	5	2	PT0600
26	6	35.3	5	2	PT0729
27	6	35.3	5	2	PT0624
28	6	35.3	5	2	PT0601
29	6	35.3	5	2	PT0672

30	6	35.3	5	2	PT0660	T-cell receptor be
31	6	35.3	5	2	PT0651	T-cell receptor be
32	6	35.3	5	2	PT0656	T-cell receptor be
33	6	35.3	5	2	PT0535	T-cell receptor be
34	6	35.3	5	2	PT0699	T-cell receptor be
35	6	35.3	5	2	PT0538	T-cell receptor be
36	6	35.3	5	2	PT0561	T-cell receptor be
37	6	35.3	5	2	PT0540	T-cell receptor be
38	6	35.3	5	2	PT0703	T-cell receptor be
39	6	35.3	5	2	PT0690	T-cell receptor be
40	6	35.3	5	2	PT0573	T-cell receptor be
41	6	35.3	5	2	PT0580	T-cell receptor be
42	6	35.3	5	2	PT0679	T-cell receptor be
43	6	35.3	5	2	S68326	blood cell protein
44	6	35.3	6	2	A61419	sarcosine dehydrog
45	6	35.3	6	2	B44510	hypothetical prote

ALIGNMENTS

RESULT 1
140697
blotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: 140697
R:Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
A:Reference number: 140697; MVID:89006280; PMID:2971595
A:Accession: 140697
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:M21922; NID:9144434

Query Match 35.3%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 3 D 3

RESULT 2
A41890
protein D - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
R:Stettan, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindqvist, B.H.
J. Bacteriol. 174, 4094-4100, 1992
A:Title: Escherichia coli K-12 and B contain functional bacteriophage P2 ogr genes.
A:Reference number: A41890; MVID:92283767; PMID:1597424
A:Accession: A41890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <SLE>
A:Cross-references: GB:M81463

Query Match 35.3%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 3
D41654

hypothetical protein (sodc 5' region) - Haemophilus parainfluenzae (fragment)
C:Species: Haemophilus parainfluenzae
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
C:Accession: D41654
R:Kroll, J.S.; Langford, P.R.; Loynds, B.M.
J. Bacteriol. 173, 7449-7457, 1991
A:Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para
A:Reference number: A41654; MUID:92041655; PMID:1938942
A:Accession: D41654
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-4 <KRO>

Query Match 35.3%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 4

A32480
A:Title: Achatina-I - giant African snail
N:Contains: Achatina-II
C:Species: Achatina fulica (giant African snail)
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
C:Accession: A32480
R:Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sur
Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A:Title: Achatina-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru
A:Reference number: A32480; MUID:89273551; PMID:2597281
A:Accession: A32480
A:Molecule type: protein
A:Residues: 1-4 <KAM>
A:Note: stereochemistry of the active form confirmed by chemical synthesis
R:Shida, I.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto
FEBS Lett. 307, 253-256, 1992
A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
(H-Gly-Phe-Ala-Asp-OH).
A:Reference number: A44691; MUID:92354723; PMID:1644179
A:Contents: annotation; X-ray crystallography, 0.85 angstroms
A:Note: Achatina-II has L-phenylalanine
C:Keywords: D-amino acid
F:2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 35.3%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 4 D 4

RESULT 5

I51049
A:Title: metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OIS>
A:Cross-references: EMBL:X80181; NID:91019799; PIDN:CA5646.1; PID:94379328

Query Match 35.3%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 2 D 2

RESULT 6

PT0271
A:Title: heavy chain CRD3 region (clone 3-103A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0271
R:Yamada, M.; Messerian, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0271
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.3%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 7

B53284
A:Title: T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity an
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: B53284
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:9233916; PIDN:AA19518.1; PID:9233918
A:Note: sequence extracted from NCBI Backbone (NCBIN:60737, NCBI:60738)
C:Keywords: T-cell receptor

Query Match 35.3%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 8

PT0696
A:Title: T-cell receptor beta chain V-D-J region (100-2N) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0696; PT0612; PT0545; PT0692; PT0552; PT0696
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0696
A:Status: translation not shown
A:Molecule type: mRNA

A:Residues: 1-4 <FE2>
 A:Experimental source: newborn thymus, strain BALB/c, 100-2N
 A:Accession: PT0612
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE2>
 A:Experimental source: newborn thymus, strain BALB/c, 111-1J
 A:Accession: PT0545
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AD
 A:Accession: PT0692
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE4>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1M
 A:Accession: PT0552
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE5>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 126-1CI
 A:Accession: PT0696
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE6>
 A:Experimental source: newborn thymus, strain BALB/c, 135-1AA
 C:Keywords: T-cell receptor

Query Match 35.3%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 4 D 4

RESULT 9

PT0711
 T-cell receptor beta chain V-D-J region (120-22) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0607; PT0674; PT0570; PT0711; PT0710
 R:Feeney, A.J.
 A:Exp. Med. 174, 115-124, 1991
 A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0607
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE1>
 A:Experimental source: newborn thymus, strain BALB/c, 120-2J
 A:Accession: PT0674
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE2>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
 A:Accession: PT0678
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE3>
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
 A:Accession: PT0570
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-4 <FE4>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
 A:Accession: PT0711
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-4 <FE5>
 A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AF and 161-2AF)

C:Keywords: T-cell receptor

Query Match 35.3%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 4 D 4

RESULT 10

A26209
 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 10-Sep-1987 #sequence_revision 10-Sep-1987 #text_change 03-Mar-1995
 C:Accession: A26209
 R:Connell, J.M.; Chung, S.I.; Whetzel, N.K.; Bradley, L.M.; Folk, J.E.
 J. Biol. Chem. 246, 1093-1098, 1971
 A:Title: Structural properties of guinea pig liver transglutaminase.
 A:Reference number: A26209; MUID:71111415; PMID:5543674
 A:Accession: A26209
 A:Molecule type: protein
 A:Residues: 1-4 <CON>
 A:Experimental source: liver
 C:Keywords: aminocyltransferase

Query Match 35.3%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 3 D 3

RESULT 11

A32516
 cholecystokinin-5 - dog
 N:Alternate names: CCK-5
 C:Species: Canis lupus familiaris (dog)
 C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
 C:Accession: A32516
 R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.
 Am. J. Physiol. 252, G272-G275, 1987
 A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
 A:Reference number: A32516; MUID:87133871; PMID:3826354
 A:Accession: A32516
 A:Molecule type: protein
 A:Residues: 1-5 <SH1>
 C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; neuropeptide
 F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 35.3%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 4 D 4

RESULT 12

C23751
 spinal cord peptide SCP-6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
 C:Accession: C23751
 R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou
 Arch. Biochem. Biophys. 240, 178-183, 1985
 A:Reference number: A23751; MUID:85250425; PMID:4015098

A:Accession: C23751
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 1-5 <HS1>
 C:Superfamily: unassigned animal peptides

Query Match 35.3%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 |
 Db 1 D 1

RESULT 13

A26830
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: A26830
 R:Reichelt, K.; Elgyo, K.; Edmonson, P.D.
 Blochem. Biophys. Res. Commun. 146, 1493-1501, 1987
 A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
 A:Reference number: A26830; PMID:87298602; PMID:3619940
 A:Accession: A26830
 A:Molecule type: Protein
 A:Residues: 1-5 <RE1>
 C:Superfamily: unassigned animal peptides
 C:Keywords: blocked amino end; pyroglutamic acid
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 35.3%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 |
 Db 3 D 3

RESULT 14

A32014
 C:Species: Escherichia coli
 C:Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
 C:Accession: A32014
 R:Imamoto, S.; Yoshio, Y.; Ohtsubo, E.
 J. Bacteriol. 170, 2749-2757, 1988
 A:Title: Identification and characterization of the products from the trax and tray genes
 A:Reference number: A32014; PMID:88227859; PMID:2836369
 A:Accession: A32014
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <INA>
 C:Genetics:
 A:Genome: plasmid
 C:Keywords: DNA binding

Query Match 35.3%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 |
 Db 3 D 3

RESULT 15

B31836
 C:Species: Rickettsia rickettsii (fragment)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999

C:Accession: B31836
 R:Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
 J. Bacteriol. 170, 4493-4500, 1988
 A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
 A:Reference number: B31836; PMID:89008059; PMID:3139629
 A:Accession: B31836
 A:Molecule type: DNA
 A:Residues: 1-5 <AND>
 A:Cross-references: GB:J03371; NID:G152455; PID:AA015030.1; PID:G4262874

Query Match 35.3%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 |
 Db 2 D 2

Search completed: June 5, 2003, 15:34:01
 Job time : 11.8182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:34:07 ; Search time 7.81818 Seconds

(Without alignments)
63.661 Million cell updates/sec

Title: US-09-150-947f-18

Perfect score: 17

Sequence: 1 XXXXXXXXXXXXD 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892.

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6	35.3	3	1	LUXE_VIBFI	P24572 vibrio flisc
2	6	35.3	4	1	ACH1_ACHFV	P35904 achatia fu
3	6	35.3	4	1	OCPI_OCTMI	P58648 octopus min
4	6	35.3	4	1	OCPI_OCTMI	P58649 octopus min
5	6	35.3	5	1	BIOA_CITFR	P13071 citrobacter
6	6	35.3	5	1	RELI_LITRU	P82070 listeria rub
7	6	35.3	5	1	TRM3_ECOLI	P13973 escherichia
8	6	35.3	5	1	UXA4_CHLTR	P38005 chlamydia t
9	6	35.3	6	1	ASP2_LACSN	P82655 lactobacill
10	6	35.3	6	1	TRP1_PSEPU	P36414 pseudomonas
11	6	35.3	7	1	ALL4_CARMA	P81807 carcius ma
12	6	35.3	7	1	ALL7_CVDPO	P82158 cydia pomon
13	6	35.3	7	1	CHOK_AICSP	P16101 alcaligenes
14	6	35.3	7	1	FAR1_HELTI	P41871 helisoma tr
15	6	35.3	7	1	FAR2_PROCL	P38498 procamburus
16	6	35.3	7	1	FARB_CALVO	P41866 calliphora
17	6	35.3	7	1	UF03_MOUSE	P38641 mus musculu
18	6	35.3	7	1	UF04_MOUSE	P38642 mus musculu
19	6	35.3	8	1	ACT1_THRAL	P18691 thunnus alb
20	6	35.3	8	1	ACT1_CARMA	P80709 carcius ma
21	6	35.3	8	1	AKH_MELML	P25423 melolontha
22	6	35.3	8	1	AL12_CARMA	P81815 carcius ma
23	6	35.3	8	1	AL18_CARMA	P81821 carcius ma
24	6	35.3	8	1	ALL4_CALVO	P41841 calliphora
25	6	35.3	8	1	ALL5_CALVO	P41840 calliphora
26	6	35.3	8	1	ALL5_CVDPO	P82156 cydia pomon
27	6	35.3	8	1	ANG2_BOTJA	Q10582 bothriops ja
28	6	35.3	8	1	CCKN_MACEU	P30369 macropus eu
29	6	35.3	8	1	COXG_RAT	P80430 rattus norv
30	6	35.3	8	1	FAR1_PANRE	P41872 panagrellus
31	6	35.3	8	1	FAR3_HOMAM	P4186 homarus ame
32	6	35.3	8	1	FAR3_CALVO	P41863 calliphora
33	6	35.3	8	1	GLOR_HUMAN	P02729 homo sapien

34	6	35.3	8	1	LCK1_LEUMA	P21140 leucophaea
35	6	35.3	8	1	LCK2_LEUMA	P21141 leucophaea
36	6	35.3	8	1	LCK3_LEUMA	P21142 leucophaea
37	6	35.3	8	1	LCK4_LEUMA	P21143 leucophaea
38	6	35.3	8	1	LCK7_LEUMA	P19989 leucophaea
39	6	35.3	8	1	LCK8_LEUMA	P19990 leucophaea
40	6	35.3	8	1	LMT2_LOCTI	P22356 locusta mlg
41	6	35.3	8	1	ORMY_ORCLI	P82455 orconectes
42	6	35.3	8	1	PLP_BRANA	P81707 brassica na
43	6	35.3	8	1	UC26_MAIZE	P80632 zea mays tm
44	6	35.3	8	1	UPA1_HUMAN	P30087 homo sapien
45	6	35.3	9	1	COM_CONVE	P83047 conus ventr

ALIGNMENTS

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RESULT 1
LUXE_VIBRI
ID LUKE_VIBRI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN LUKE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=568;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; Pubmed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Weighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.;"
RL J. Bacteriol. 172:6797-6802(1990).
CC - FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC - CATALYTIC ACTIVITY: ATP + an acid + protein -> AMP + diphosphate +
CC an acyl-protein thioester.
CC - PATHWAY: Bioluminescent fatty acid reduction system; second step.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62812; ; NOT_ANNOTATED_CDS.
KW Bioluminescence; Ligase.
FT NON_TER
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CMC64;

Query Match 35.3%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 3 D 3

RESULT 2
ACH1_ACHFU STANDARD; PRT; 4 AA.
ID ACH1_ACHFU
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

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DT 15-JUN-1998 (Rel. 36, last annotation update)
 DE Achatin-I.
 OS Achatina fulica (giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Achatinaceae; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN-Perussac; TISSUE-Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kametani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Fumase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Ll P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.,
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 fulica Ferussac containing a D-amino acid residue.";
 RT Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN-Perussac; TISSUE-Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 Achatina fulica, and its possible function.";
 RT Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 D-amino acid residue.";
 RT Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 CC DR PIR. A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD.RES 2
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C81000000 CRC64;
 D-PHENYALANINE.
 Query Match 35.3%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4
 RESULT 3
 ID OCP1_OCTMI STANDARD; PRT; 4 AA.
 AC P58648;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 CC Invertebrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE-Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 Octopus minor.";
 RT Peptides 21:623-630(2000).
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
 inotropic effects on the heart. Ocp-4 is a 1000 time less
 active than Ocp-3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD.RES 2
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B81000000 CRC64;
 D-SERINE (IN OCP-4).
 Query Match 35.3%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4

CC Inotropic effects on the heart. Ocp-2 is a 1000 time less
 active than Ocp-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD.RES 2
 SQ SEQUENCE 4 AA; 394 MW; 6AA879C81000000 CRC64;
 D-PHENYALANINE.
 Query Match 35.3%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4
 RESULT 4
 ID OCP3_OCTMI STANDARD; PRT; 4 AA.
 AC P58649;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Cardioactive peptides Ocp-3/Ocp-4.
 OS Octopus minor (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 CC Invertebrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE-Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 Octopus minor.";
 RT Peptides 21:623-630(2000).
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
 inotropic effects on the heart. Ocp-4 is a 1000 time less
 active than Ocp-3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD.RES 2
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B81000000 CRC64;
 D-SERINE (IN OCP-4).
 Query Match 35.3%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4
 RESULT 5
 ID BIOA_CITFR STANDARD; PRT; 5 AA.
 AC P13071;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
 (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
 amino transferase) (Fragment).
 CC Citrobacter freundii.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE:89006280; PubMed-2971595;
 RA Shiuan D., Campbell A.;
 RT "transcriptional regulation and gene arrangement of *Escherichia coli*,
 RT *Citrobacter freundii* and *Salmonella typhimurium* biotin operons.";
 RL Gene 67:203-211(1988).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate -> S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: Biotin biosynthesis.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
 CC -----
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 CC -----
 CC EMBL: M21922; NOT_ANNOTATED_CDS.
 DR Interpro: IPR000934; AminoTran_3.
 DR PROSITE: PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
 KM Biotin biosynthesis; Transferase; Amino transferase;
 KM Pyridoxal phosphate.
 FT NON_TER 5
 SQ SEQUENCE 5 AA: 582 MW: 66AAB1B1A6F00000 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 5;
 Db Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 4 D 4
 RESULT 6
 RE1_LITRU STANDARD; PRT; 5 AA.
 AC P82070;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 1.1.
 OS *Litoria rubella* (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodytidae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
 RT 'The structure of new peptides from the Australian red tree frog *Litoria rubella*, the skin peptide profile as a probe for the study of evolutionary trends of amphibians.';
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MS-598; METHOD-FAB.
 KM Amphibian skin.
 SQ SEQUENCE 5 AA: 598 MW: 6DD9C9CAB2A00000 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 5;
 Db Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
 Db 2 D 2
 RESULT 7
 TRM3_ECOLI STANDARD; PRT; 5 AA.
 AC P13973;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Trm protein (Fragment).
 GN TRAM.
 OS *Escherichia coli*.
 OC Plasmid IncF1 R100.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:88227859; PubMed-2836369;
 RA Inamoto S., Yoshioke Y., Ohtsubo E.;
 RT "Identification and characterization of the products from the trmJ and trm genes of plasmid R100.";
 RL J. Bacteriol. 170:2749-2757(1988).
 CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
 CC -----
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 CC -----
 CC EMBL: M20941; NOT_ANNOTATED_CDS.
 DR PIR: A32014; A32014.
 KM Conjugation; Plasmid; DNA-binding.
 FT NON_TER 1
 SQ SEQUENCE 5 AA: 634 MW: 6B1B1AA443500000 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 5;
 Db Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 3 D 3
 RESULT 8
 UX44_CHLTR STANDARD; PRT; 5 AA.
 AC P38005;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS *Chlamydia trachomatis*.
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christensen G., Birkelund S., Vitreou E., Ratti G., Pallini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN

CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
 DR Stena-2DPAGE; P38005; -.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;
 Query Match
 Best Local Similarity 35.3%; Score 6; DB 1; Length 5;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4
 RESULT 9
 ASP2_LACSN STANDARD; PRT; 6 AA.
 ID ASP2_LACSN
 AC P82655;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acid shock protein 2 (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 CC NCBI_Taxid=1625;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=CBI;
 RX MEDLINE=21322712; PubMed=11429463;
 RA De Angelis M., Bini L., Pallini V., Coccocelli P.S., Gobetti M.;
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";
 RL Microbiology 147:1863-1873(2001).
 CC -1- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;
 Query Match
 Best Local Similarity 35.3%; Score 6; DB 1; Length 6;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 6 D 6
 RESULT 10
 TRPI_PSEPU STANDARD; PRT; 6 AA.
 ID TRPI_PSEPU
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TRPA operon transcriptional activator (Fragment).
 GN TRPI.
 OS Pseudomonas putida.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 CC NCBI_Taxid=303;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=PRGI C15;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas putida.";
 RT Blochmle 71:521-531(1989).
 CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRAP OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: X13299; CAA31660.1;
 DR InterPro: IPR000847; HTH_LYSR.
 DR PROSITE: PS00044; HTH_LYSR_FAMILY: PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
 Query Match
 Best Local Similarity 35.3%; Score 6; DB 1; Length 6;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4
 RESULT 11
 ALI4_CARMA STANDARD; PRT; 7 AA.
 ID ALI4_CARMA
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carinustatin 4.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Brachyura; Eubrachyura; Portunioidea; Portunidae; Carcinus.
 CC NCBI_Taxid=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion.
 RX MEDLINE=98121193; PubMed=9461285;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTANSITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 783 MW; 672879CDB476AC0 CRC64;
 Query Match
 Best Local Similarity 35.3%; Score 6; DB 1; Length 7;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 1 D 1
 RESULT 12
 ALI7_CYPDPO STANDARD; PRT; 7 AA.
 ID ALI7_CYPDPO
 AC P82158;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydistastatin 7.
 OS Cydia pomonella (Coddling moth).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

OC Dityrphia: Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=92600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dave H., Johnson A.H., Maestre J.-L., Scott A.G., Winstanley D.,
 RT "Leptopterian peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLANOSTATIN FAMILY.
 CC Neuropeptide: Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 D 12
 4 D 4
 RESULT 13
 CHOX_ALCSP STANDARD; PRT; 7 AA.
 ID ID
 AC P16101;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Choline oxidase (EC 1.1.3.17) (Fragment).
 OS Alcaligenes sp.
 OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 CC Alcaligenes.
 OX NCBI_TaxID=512;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81006769; PubMed=6997283;
 RA Ohta-Fukuyama M., Miyake Y., Eml S., Yamano T.;
 RT "Identification and properties of the prosthetic group of choline
 oxidase from Alcaligenes sp.";
 RL J. Biochem. 88:197-203(1980).
 CC -1- CATALYTIC ACTIVITY: Choline + O(2) -> betaine aldehyde + H(2)O(2).
 DR PIR: A15398; A15398.
 KM Oxidoreductase.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 839 MW; 7A15B1E457644AC0 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 D 12
 1 D 1
 RESULT 14
 FAR1_HELTI STANDARD; PRT; 7 AA.
 ID ID
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GDFPLRF-amide.
 OS Helisoma trivolvis (Snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
 CC Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 FT TISSUE-Kidney;

RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC THE KIDNEY, MANTLE AND SKIN.
 CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide: Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 D 12
 2 D 2
 RESULT 15
 FAR2_PROCL STANDARD; PRT; 7 AA.
 ID ID
 AC P38498;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardiac excitatory FMRFamide homolog DF2.
 OS Procambarus clarkii (Red swamp crayfish).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Astacidae; Astacoidae; Cambaridae; Procambarus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebruge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 pericardial organs.";
 RL Peptides 14:137-143(1993).
 CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide: Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
 QY Query Match 35.3%; Score 6; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 12 D 12
 1 D 1
 Search completed: June 5, 2003, 15:56:35
 Job time : 7.81818 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:32:58 ; Search time 34.9091 Seconds
(without alignments)
70.829 Million cell updates/sec

Title: US-09-150-947F-18
Perfect score: 17
Sequence: 1 xxxxxxxxxxxd 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	35.3	5	2	P83073 bacillus ce
2	6	35.3	7	2	O07354 synechococ
3	6	35.3	7	5	P83274 macrobrachi
4	6	35.3	7	6	O28742 oryctolagus
5	6	35.3	7	10	O49223 glycine max
6	6	35.3	7	11	O63480 rattus norv
7	6	35.3	7	11	O55184 rattus norv
8	6	35.3	8	2	O92189 neisseria m
9	6	35.3	8	2	O85406 coxiella bu
10	6	35.3	8	2	O9RQ57 buchiera ap
11	6	35.3	8	2	O9RQ49 buchiera ap
12	6	35.3	8	2	O9R772 escherichia
13	6	35.3	8	2	P72279 rhodococcus
14	6	35.3	8	2	O56759 xanthobacte
15	6	35.3	8	2	P83158 anabaena sp
16	6	35.3	8	2	O51594 escherichia

17	6	35.3	8	2	O93SR0	O93SR0 staphylococ
18	6	35.3	8	2	P83152	P83152 anabaena sp
19	6	35.3	8	2	O9R3X0	O9R3X0 planktothri
20	6	35.3	8	2	O53790	O53790 streptococc
21	6	35.3	8	2	O8RSR3	O8RSR3 lactobacilli
22	6	35.3	8	2	O9HDS4	O9HDS4 aspergillus
23	6	35.3	8	3	O9URB9	O9URB9 saccharomyc
24	6	35.3	8	4	O9P285	O9P285 homo sapien
25	6	35.3	8	4	O9UJ50	O9UJ50 homo sapien
26	6	35.3	8	4	O9HAD3	O9HAD3 homo sapien
27	6	35.3	8	4	O15895	O15895 homo sapien
28	6	35.3	8	4	O15900	O15900 homo sapien
29	6	35.3	8	4	O15902	O15902 homo sapien
30	6	35.3	8	4	O9UMC7	O9UMC7 homo sapien
31	6	35.3	8	4	O9UMH9	O9UMH9 homo sapien
32	6	35.3	8	4	O9UDZ4	O9UDZ4 homo sapien
33	6	35.3	8	4	O9P0K3	O9P0K3 homo sapien
34	6	35.3	8	4	O9BYR5	O9BYR5 homo sapien
35	6	35.3	8	5	O9NMK5	O9NMK5 toxoplasma
36	6	35.3	8	5	O9UB13	O9UB13 albinaria h
37	6	35.3	8	5	O94695	O94695 physarum po
38	6	35.3	8	5	P83195	P83195 perkinsus a
39	6	35.3	8	5	P83275	P83275 macrobrachi
40	6	35.3	8	5	P83316	P83316 penaeus mon
41	6	35.3	8	5	O9TWH6	O9TWH6 perinelets
42	6	35.3	8	5	P82687	P82687 periplaneta
43	6	35.3	8	5	P82687	P82687 periplaneta
44	6	35.3	8	6	O9T778	O9T778 canis famli
45	6	35.3	8	6	O8WNS1	O8WNS1 bos taurus

ALIGNMENTS

RESULT 1
P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TREMUREL.18, Created)
DT 01-OCT-2001 (TREMUREL.18, Last sequence update)
DT 01-OCT-2001 (TREMUREL.18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/clostridium group; Bacilliales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID:1396;
RN [1]
RP
SEQUENCE.
RC STRAIN-NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER
SQ SEQUENCE 5 AA; 623 MW; 6801AAA336F00000 CRC64;
Query Match 35.3%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 12 D 12
Db 3 D 3
RESULT 2
O07354 PRELIMINARY; PRT; 7 AA.
AC O07354;
DT 01-JUN-1997 (TREMUREL.04, Created)
DT 01-JUN-1997 (TREMUREL.04, Last sequence update)
DT 01-DEC-2001 (TREMUREL.19, Last annotation update)
DE NifK (Fragment).
GN NifK.
OS synechococcus sp. (strain PCC 8801 / Rf-1) (Cyanothecae PCC 8801).

OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 OX NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RF-1;
 RX MEDLINE-99231861; PubMed-10217509;
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic
 RT nitrogen-fixing unicellular cyanobacterium *Synechococcus* sp. strain
 RF-1.";
 RL Microbiology 145:743-753(1999).
 DR EMBL: AF003700; AAC35193.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
 Query Match 35.3%; Score 6; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 4 D 4

RESULT 3
 ID P83274 PRELIMINARY; PRT; 7 AA.
 AC P83274;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DE FMRamide-1-like neuropeptide FLP1 (DRNFLR-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidae; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-EYESTALK;
 RA Stichgornigul P., Sarathongkum W., Jaldeschoey S., Longyant S.,
 RA Stichgornigul W.;
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn *Macrobrachium rosenbergii*.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -1- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 7 7
 FT SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;
 SQ
 Query Match 35.3%; Score 6; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 1 D 1

RESULT 4
 ID Q28742 PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS *Oryctolagus cuniculus* (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84221901; PubMed-6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL: K01698; AAA31415.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;
 Query Match 35.3%; Score 6; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 5 D 5

RESULT 5
 ID 049223 PRELIMINARY; PRT; 7 AA.
 AC 049223;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE HMG-1-like protein (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. ESSEX; TISSUE=ROOT;
 RX MEDLINE-91367679; PubMed-1891369;
 RA Laux T., Goldberg R.B.;
 RT "A plant DNA binding protein shares highly conserved sequence motifs
 RT with HMG-box proteins.";
 RL Nucleic Acids Res. 19:4769-4769(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. ESSEX; TISSUE=ROOT;
 RA Mahalingam R., Knapp H.T.;
 RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF047050; AAC03556.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;
 Query Match 35.3%; Score 6; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 D 12
 DB 5 D 5

RESULT 6
 ID 063480 PRELIMINARY; PRT; 7 AA.
 AC 063480;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TR4-NS orphan receptor (Fragment).
 GN TR4.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96198747; PubMed-8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RT Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain";
 RT domainology 137:1562-1571(1996).
 DR EMBL: U59125; AAB02827.1; -.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;
 Query Match 35.3%; Score 6; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 6 D 6
 RESULT 7
 ID 055184 PRELIMINARY; PRT; 7 AA.
 AC 055184;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Orphan receptor TR4-NS (Fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-96198747; PubMed-8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RT Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain";
 RT domainology 137:1562-1571(1996).
 DR EMBL: U59454; AAB91433.1; -.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 7 AA; 663 MW; 6DDA8A787EB05350 CRC64;
 Query Match 35.3%; Score 6; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 6 D 6
 RESULT 8
 ID 0921E9 PRELIMINARY; PRT; 8 AA.
 AC 0921E9;
 DT 01-MAY-1999 (TREMblrel. 10, Created)

DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE Carbamoyl-phosphate synthase subunit B (Fragment).
 GN CARB.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_Taxid-487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1527;
 RX MEDLINE-95291461; PubMed-7773412;
 RA Lawson F.S., Billowes F.M., Dillon J.A.;
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
 RT gonorrhoeae includes a large, variable intergenic sequence which is
 RT also present in other Neisseria species";
 RT Microbiology 141:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1527;
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
 RT "Complexity of the variable sequence between the carbamoyl-phosphate
 RT synthase genes of Neisseria species";
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF029361; AAC78449.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CRC64;
 Query Match 35.3%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 6 D 6
 RESULT 9
 ID 085406 PRELIMINARY; PRT; 8 AA.
 AC 085406;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 OS Coxiella burnetii.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 OC Coxiella group; Coxiella.
 OC NCBI_Taxid-777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NINE MILE PHASE I;
 RX MEDLINE-98348442; PubMed-9683477;
 RA Williams H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 RT Coxiella burnetii";
 RT J. Bacteriol. 180:3816-3822(1998).
 DR EMBL: AF064963; AAD09947.1; -.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA45372727 CRC64;
 Query Match 35.3%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 6 D 6
 RESULT 10
 ID 09RO57 PRELIMINARY; PRT; 8 AA.
 AC 09RO57

AC O9R057:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN Nifs.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 RT compositions."
 RL EMBL: AF130812; AAF13797.1; -.
 DR EMBL: AF130812; AAF13797.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;

Query Match 35.3%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 8 D 8

RESULT 11

O9R049 PRELIMINARY; PRT; 8 AA.
 AC O9R049:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN Nifs.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 RT compositions."
 RL EMBL: AF130814; AAF13805.1; -.
 DR EMBL: AF130814; AAF13805.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match 35.3%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 8 D 8

RESULT 12

O9R7T2 PRELIMINARY; PRT; 8 AA.
 AC O9R7T2:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 GN YOF6.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horinchi T.;
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
 RT to the 12,7-28.0 min Region on the Linkage Map."
 RL DNA Res. 3:137-155(1996).
 DR EMBL: D90705; BAA35310.1; -.
 FT Hypothetical protein.
 KW NON_TER
 SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 35.3%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 1 D 1

RESULT 13

P72279 PRELIMINARY; PRT; 8 AA.
 AC P72279:
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Biphenyl dioxygenase (Fragment).
 GN BphB.
 OS Rhodococcus globerulus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Rhodococcus.
 OX NCBI_TaxID=33008;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95255652; PubMed=7737502;
 RA Asturias J.A., Diaz E., Timmis K.N.;
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
 RT positive bacterium Rhodococcus globerulus p6 to multicomponent
 RT dioxygenases of gram-negative bacteria."
 RL Gene 136:11-18(1995).
 DR EMBL: X80041; CAA56350.1; -.
 KW Dioxygenase.
 FT NON_TER
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 35.3%; Score 6; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
 DB 5 D 5

RESULT 14

O56759 PRELIMINARY; PRT; 8 AA.
 AC O56759:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Halocacid dehalogenase (Fragment).
 GN DHB.
 OS Xanthobacter autotrophicus.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Hyphomicrobium group; Xanthobacter.

OX NCBI_TaxID-280;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-GJ10, AND CV. M50;

RK MEDLINE-95173113; PubMed-7868610;

RA Van der Ploeg J., Willemse M., van Hall G., Janssen D.B.;

RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to

RT activation and mobilization of the haloacetate dehalogenase gene by

RT insertion element IS1247";

RL J. Bacteriol. 177:1348-1356(1995).

DR EMBL; X84038; CAA58857.1; -.

FT NON_TER

FT NON_TER

SQ SEQUENCE

8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match

Best Local Similarity 35.3%; Score 6; DB 2; Length 8;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12

DB 8 D 8

RESULT 15

P83158

ID P83158

AC P83158

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa

DE polypeptide) (PSI-C) (Fragment).

OS Anabaena sp. (strain L31).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.

OX NCBI_TaxID-29412;

RN [1]

RP SEQUENCE.

RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;

RL Submitted (OCT-2001) to the SWISS-PROT data bank.

CC -I- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS PA AND PB OF THE

CC PHOTOSYSTEM I COMPLEX.

CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -I- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF

CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.

DR InterPro; IPR001450; 4Fe4S_ferredoxin.

DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; PARTIAL.

KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.

FT NON_TER

FT NON_TER

SQ SEQUENCE

8 AA; 962 MW; C5B8505322D1A1F5 CRC64;

Query Match

Best Local Similarity 35.3%; Score 6; DB 2; Length 8;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12

DB 8 D 8

Search completed: June 5, 2003, 15:55:45
 Job time : 34.9091 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:29:17 ; Search time 123.182 Seconds

(without alignments)
52.340 Million cell updates/sec

Title: US-09-150-947F-13

Perfect score: 31

Sequence: 1 KXXXTXQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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25: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	77.4	204	22	US-09-869-136-9
2	24	77.4	209	21	US-09-791-537-103693
3	24	77.4	209	21	US-09-791-537-103695
4	24	77.4	209	21	US-09-791-537-103701
5	24	77.4	209	21	US-09-791-537-103704
6	24	77.4	209	21	US-09-791-537-103705

7	24	77.4	209	21	US-09-791-537-103706
8	24	77.4	209	21	US-09-791-537-103708
9	24	77.4	209	21	US-09-791-537-103712
10	24	77.4	209	21	US-09-791-537-103715
11	24	77.4	209	21	US-09-791-537-103717
12	24	77.4	209	21	US-09-791-537-103719
13	24	77.4	209	21	US-09-791-537-103720
14	24	77.4	209	21	US-09-791-537-103729
15	24	77.4	209	21	US-09-791-537-103732
16	24	77.4	209	21	US-09-791-537-103736
17	24	77.4	209	21	US-09-791-537-103738
18	24	77.4	209	21	US-09-791-537-103740
19	24	77.4	209	21	US-09-791-537-103749
20	24	77.4	209	21	US-09-791-537-120755
21	24	77.4	209	21	US-09-791-537-137418
22	24	77.4	210	21	US-09-791-537-85735
23	24	77.4	233	22	US-09-869-136-2
24	24	77.4	256	21	US-09-791-537-86827
25	24	77.4	256	21	US-09-791-537-88724
26	24	77.4	256	21	US-09-791-537-97492
27	24	77.4	278	20	US-09-675-784A-11175
28	24	77.4	603	21	US-09-791-537-25751
29	24	77.4	603	21	US-09-791-537-41676
30	24	77.4	604	21	US-09-791-537-12679
31	24	77.4	604	21	US-09-791-537-12679
32	24	77.4	955	21	US-09-791-537-126252
33	23	74.2	17	8	US-08-491-746-6
34	23	74.2	17	19	US-09-555-115A-30
35	23	74.2	17	19	US-09-555-115A-31
36	23	74.2	17	19	US-09-555-115A-32
37	23	74.2	17	21	US-09-708-008B-6
38	23	74.2	24	1	PCT-US00-16680A-20
39	23	74.2	24	12	US-08-838-413-20
40	23	74.2	24	17	US-09-335-581-20
41	23	74.2	24	17	US-09-335-581A-20
42	23	74.2	24	17	US-09-335-621B-20
43	23	74.2	24	17	US-09-335-581-20
44	23	74.2	29	1	PCT-US01-00663-32245
45	23	74.2	29	22	US-09-864-761-43487

ALIGNMENTS

RESULT 1
US-09-869-136-9
; Sequence 9, Application US/09869136
; GENERAL INFORMATION:
; APPLICANT: FRASER, JOHN DAVID
; APPLICANT: PROF, THOMAS
; TITLE OF INVENTION: SUPERANTIGENS
; FILE REFERENCE: 3911-8
; CURRENT APPLICATION NUMBER: US/09/869,136
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/NZ99/00228
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: NZ 333589
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-869-136-9

Query Match
Best local Similarity 77.4%; Score 24; DB 22; Length 204;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 KXXXTXQEXD 10
DB 123 KTTVTAAQED 132

RESULT 2
US-09-791-537-103693
; Sequence 103693, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103693
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103693

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Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 125 KTVTAQIED 134

RESULT 3
US-09-791-537-103695
; Sequence 103695, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103695
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103695

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 125 KTVTAQIED 134

RESULT 4
US-09-791-537-103701
; Sequence 103701, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103701
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103701

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 125 KTVTAQIED 134

RESULT 5
US-09-791-537-103704
; Sequence 103704, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; SEQ ID NO 103704
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103704

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 125 KTVTAQIED 134

RESULT 6
US-09-791-537-103705
; Sequence 103705, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; SEQ ID NO 103705
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103705

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
| | | |
DB 125 KTVTAQIED 134


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RESULT 7
US-09-791-537-103706
; Sequence 103706, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103706
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103706

Query Match
Best Local Similarity 50.0%; Score 24; DB 21; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
DB 125 KTTVTAQXND 134

RESULT 8
US-09-791-537-103708
; Sequence 103708, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103708
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103708

Query Match
Best Local Similarity 50.0%; Score 24; DB 21; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
DB 125 KTTVTAQXND 134

RESULT 9
US-09-791-537-103712
; Sequence 103712, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103712
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103712

Query Match
Best Local Similarity 50.0%; Score 24; DB 21; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
DB 125 KTTVTAQXND 134

RESULT 10
US-09-791-537-103715
; Sequence 103715, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103715

Query Match
Best Local Similarity 50.0%; Score 24; DB 21; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
DB 125 KTTVTAQXND 134

RESULT 11
US-09-791-537-103717
; Sequence 103717, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103717
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103717

Query Match
Best Local Similarity 50.0%; Score 24; DB 21; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
DB 125 KTTVTAQXND 134
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RESULT 12
US-09-791-537-103719
; Sequence 103719, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103719
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103719

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
| | | | |
Db 125 KTVTAQED 134

RESULT 13
US-09-791-537-103720
; Sequence 103720, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103720
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103720

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
| | | | |
Db 125 KTVTAQED 134

RESULT 14
US-09-791-537-103729
; Sequence 103729, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103729

; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103729

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
| | | | |
Db 125 KTVTAQED 134

RESULT 15
US-09-791-537-103733
; Sequence 103733, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103733
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103733

Query Match 77.4%; Score 24; DB 21; Length 209;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQEXD 10
| | | | |
Db 125 KTVTAQED 134

Search completed: June 5, 2003, 15:47:34
Job time : 124.182 secs

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OM protein - protein search, using SW model

Run on: June 5, 2003, 15:31:47 ; Search time 28.4848 Seconds
(without alignments)
74.544 Million cell updates/sec

Title: US-09-150-947f-13

Perfect score: 31

Sequence: 1 KXXRYQEXD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1012620 seqs, 212337834 residues

Total number of hits satisfying chosen parameters: 1012620

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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7: /cgn2_6/pdata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	77.4	14	6	US-10-172-425B-33
2	24	77.4	278	5	US-09-675-784A-11175
3	23	74.2	14	6	US-10-172-425B-37
4	23	74.2	115	5	US-09-134-000C-6190
5	23	74.2	115	5	US-09-134-000C-6190
6	23	74.2	134	6	US-10-424-599-184221
7	23	74.2	228	6	US-10-203-536-1
8	23	74.2	266	5	US-09-751-708A-12
9	23	74.2	281	6	US-10-424-599-179861
10	23	74.2	324	7	US-60-440-068-124
11	23	74.2	627	6	US-10-431-652-7705
12	22	71.0	10	5	US-09-150-947F-3
13	22	71.0	10	5	US-09-150-947F-4
14	22	71.0	10	6	US-10-172-425B-3
15	22	71.0	10	6	US-10-172-425B-4
16	22	71.0	12	5	US-09-150-947F-1
17	22	71.0	12	5	US-09-150-947F-2
18	22	71.0	12	6	US-10-172-425B-2
19	22	71.0	12	6	US-10-172-425B-1
20	22	71.0	12	6	US-10-172-425B-2
21	22	71.0	12	7	US-60-458-305-26
22	22	71.0	13	7	US-60-458-305-29
23	22	71.0	13	5	US-09-150-947F-5
24	22	71.0	13	5	US-09-150-947F-6
25	22	71.0	13	5	US-09-150-947F-11
26	22	71.0	13	6	US-10-172-425B-5

27	22	71.0	13	6	US-10-172-425B-6	Sequence 6, App11
28	22	71.0	13	6	US-10-172-425B-11	Sequence 11, App1
29	22	71.0	14	5	US-09-150-947F-9	Sequence 9, App1
30	22	71.0	14	5	US-09-150-947F-10	Sequence 10, App1
31	22	71.0	14	6	US-10-172-425B-9	Sequence 9, App1
32	22	71.0	14	6	US-10-172-425B-10	Sequence 10, App1
33	22	71.0	14	6	US-10-172-425B-13	Sequence 13, App1
34	22	71.0	14	6	US-10-172-425B-15	Sequence 15, App1
35	22	71.0	14	6	US-10-172-425B-26	Sequence 26, App1
36	22	71.0	14	6	US-10-172-425B-27	Sequence 27, App1
37	22	71.0	14	6	US-10-172-425B-36	Sequence 36, App1
38	22	71.0	14	6	US-10-172-425B-42	Sequence 42, App1
39	22	71.0	14	6	US-10-172-425B-44	Sequence 44, App1
40	22	71.0	14	6	US-10-172-425B-45	Sequence 45, App1
41	22	71.0	14	6	US-10-172-425B-46	Sequence 46, App1
42	22	71.0	14	6	US-10-172-425B-47	Sequence 47, App1
43	22	71.0	14	6	US-10-172-425B-50	Sequence 50, App1
44	22	71.0	16	6	US-10-172-425B-14	Sequence 14, App1
45	22	71.0	24	5	US-09-150-947F-7	Sequence 7, App1

ALIGNMENTS

```
RESULT 1
US-10-172-425B-33
; Sequence 33, Application US/10172425B
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172.425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-172-425B-33
Query Match 77.4%; Score 24; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 KXXRYQEXD 10
Db 5 KTVTAQED 14
RESULT 2
US-09-675-784A-11175
; Sequence 11175, Application US/09675784A
; GENERAL INFORMATION:
; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIMER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORR
; APPLICANT: ZENG, QIANDONG
; APPLICANT: GREENE, JONATHAN R.
; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
; FILE REFERENCE: 2976-4020U51
; CURRENT APPLICATION NUMBER: US/09/675,784A
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CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/156,338
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 13925
SEQ ID NO 11175
LENGTH: 278
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-675-784A-11175

Query Match 77.4%; Score 24; DB 5; Length 278;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 126 KSDTDOESD 135

RESULT 3
US-10-172-425B-37
Sequence 37, Application US/10172425B
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Arad, Gila
TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCF-USA-A-A 066031.0164
CURRENT APPLICATION NUMBER: US/10/172,425B
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 09/150,947
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCF/1197/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-172-425B-37

Query Match 74.2%; Score 23; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 5 KSVTAQELD 14

RESULT 4
US-09-134-000C-6190
Sequence 6190, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6190
LENGTH: 115
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6190

Query Match 74.2%; Score 23; DB 5; Length 115;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 85 KKFSTQEVD 94

RESULT 5
US-09-134-000C-6190
Sequence 6190, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6190
LENGTH: 115
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6190

Query Match 74.2%; Score 23; DB 5; Length 115;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 85 KKFSTQEVD 94

RESULT 6
US-10-424-599-184221
Sequence 184221, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(33223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 184221
LENGTH: 134
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_137368C.1.pep
US-10-424-599-184221

Query Match 74.2%; Score 23; DB 6; Length 134;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 21 KTHDSQELD 30

RESULT 7
US-10-203-536-1
Sequence 1, Application US/10203536
GENERAL INFORMATION:

APPLICANT: LEE, Hong-Kyun
APPLICANT: PARK, Yong-Ho
APPLICANT: HAN, Kyu-Boem
APPLICANT: CHANG, Byoung-Sun
APPLICANT: LEE, Yong-Jun
TITLE OF INVENTION: Staphylococcal Enterotoxin SEC-SER, Expression Vector and Host Cell
FILE OF INVENTION: Production Method Thereof, and Manufacturing Method of Vaccine
FILE REFERENCE: 0808-0329P
CURRENT FILING DATE: 2002-08-12
CURRENT APPLICATION NUMBER: US/10/203,536
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: PCT/KR00/01241
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: KR 2000-0007612
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 228
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Staphylococcal enterotoxin SEC-SER
US-10-203-536-1

Query Match 74.2%; Score 23; DB 6; Length 228;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
| | | | |
Db 140 KKSXTAQELD 149

RESULT 8
US-09-751-708A-12
Sequence 12, Application US/09/51708A
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/173,371
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match 74.2%; Score 23; DB 5; Length 266;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
| | | | |
Db 178 KKSXTAQELD 187

RESULT 9
US-10-424-599-179861
Sequence 179861, Application US/10/424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 179861
LENGTH: 281
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_13342C.1.pap
US-10-424-599-179861

Query Match 74.2%; Score 23; DB 6; Length 281;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
| | | | |
Db 176 KKSXTAQELD 185

RESULT 10
US-60-440-068-124
Sequence 124, Application US/60/440068
GENERAL INFORMATION:
APPLICANT: MADLER, STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGTH: 324
TYPE: PRT
ORGANISM: Homo sapiens
US-60-440-068-124

Query Match 74.2%; Score 23; DB 7; Length 324;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 KXXXTXQXND 10
| | | | |
Db 193 KKSXTAQELD 202

RESULT 11
US-10-431-652-7705
Sequence 7705, Application US/10/431652
GENERAL INFORMATION:
APPLICANT: Breton, Gary L.
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PAT03-08
CURRENT APPLICATION NUMBER: US/10/431,652
CURRENT FILING DATE: 2003-05-06
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 09/328,352
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7705
LENGTH: 627
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-10-431-652-7705

Query Match 74.2%; Score 23; DB 6; Length 627;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 355 KSKATVQEXD 364

RESULT 12
US-09-150-947F-3

```

; Sequence 3, Application US/09150947F
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS ANTAGONISTS VACCINES
; FILE REFERENCE: A31967-PCT-USA-A 066031.0102
; CURRENT APPLICATION NUMBER: US/09/150,947F
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947F-3

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Query Match 71.0%; Score 22; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKKATVQEXD 10

RESULT 13

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US-09-150-947F-4
; Sequence 4, Application US/09150947F
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS ANTAGONISTS VACCINES
; FILE REFERENCE: A31967-PCT-USA-A 066031.0102
; CURRENT APPLICATION NUMBER: US/09/150,947F
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947F-4

```

Query Match 71.0%; Score 22; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKKATVQEXD 10

RESULT 14

```

US-10-172-425B-3
; Sequence 3, Application US/10172425B
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila

```

```

; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-3

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Query Match 71.0%; Score 22; DB 6; Length 10;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKKATVQEXD 10

RESULT 15

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US-10-172-425B-4
; Sequence 4, Application US/10172425B
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-4

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Query Match 71.0%; Score 22; DB 6; Length 10;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXXXTXQEXD 10
DB 1 KKKATVQEXD 10

Search completed: June 5, 2003, 15:52:21
Job time : 32.488 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:29:17 ; Search time 123.182 seconds

(without alignments)
52.340 Million cell updates/sec

Title: US-09-150-947f-14

Perfect score: 26

Sequence: 1 KXXXXXXIXD 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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12: /cgn2_6/ptodata/1/paa/US17_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US18_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US19_COMB.pep.*
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16: /cgn2_6/ptodata/1/paa/US21_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US26_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US27_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US28_COMB.pep.*
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26: /cgn2_6/ptodata/1/paa/US31_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US32_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	73.1	310	27	US-60-360-039-12686
2	19	73.1	358	21	US-09-733-089-16924
3	19	73.1	358	22	US-09-816-660-16924
4	19	73.1	378	19	US-09-513-996A-43459
5	19	73.1	378	21	US-09-708-427-18784
6	19	73.1	378	21	US-09-791-537-114720

7	19	73.1	378	27	US-60-356-051-2815	Sequence 2815, Ap
8	18	69.2	35	26	US-10-221-279-10068	Sequence 10068, A
9	18	69.2	43	1	PCT-US99-22853B-42	Sequence 42, Appl
10	18	69.2	46	1	PCT-US00-07527-111	Sequence 111, Appl
11	18	69.2	46	1	PCT-US00-07527-112	Sequence 112, Appl
12	18	69.2	54	1	PCT-US99-22853B-41	Sequence 41, Appl
13	18	69.2	79	1	PCT-US99-22853B-40	Sequence 40, Appl
14	18	69.2	87	15	US-09-134-000-5378	Sequence 5378, Ap
15	18	69.2	89	21	US-09-758-472-8508	Sequence 8508, Ap
16	18	69.2	89	26	US-10-235-926-8508	Sequence 8508, Ap
17	18	69.2	100	19	US-09-565-177A-13	Sequence 13, Appl
18	18	69.2	100	21	US-09-732-210-1170	Sequence 1170, Ap
19	18	69.2	100	21	US-09-791-537-23478	Sequence 23478, A
20	18	69.2	100	27	US-60-169-340-1170	Sequence 1170, Ap
21	18	69.2	122	20	US-09-617-681A-4242	Sequence 4242, Ap
22	18	69.2	131	21	US-09-708-427-46061	Sequence 46061, A
23	18	69.2	140	16	US-09-248-766-25982	Sequence 25982, A
24	18	69.2	140	27	US-60-096-409-25982	Sequence 25982, A
25	18	69.2	141	20	US-09-617-681A-4241	Sequence 4241, Ap
26	18	69.2	152	19	US-09-565-177A-4	Sequence 4, Appl
27	18	69.2	152	19	US-09-565-177A-12	Sequence 12, Appl
28	18	69.2	152	19	US-09-565-177A-6	Sequence 6, Appl
29	18	69.2	160	21	US-09-708-427-20661	Sequence 20661, A
30	18	69.2	171	21	US-09-708-427-20661	Sequence 20660, A
31	18	69.2	173	1	PCT-US01-08631-50628	Sequence 50628, A
32	18	69.2	200	22	US-09-809-391-495	Sequence 495, App
33	18	69.2	200	22	US-09-882-171-495	Sequence 495, App
34	18	69.2	200	25	US-10-164-861-495	Sequence 495, App
35	18	69.2	205	27	US-60-389-987-655	Sequence 655, App
36	18	69.2	205	27	US-60-412-418-655	Sequence 655, App
37	18	69.2	206	27	US-60-389-987-2179	Sequence 2179, Ap
38	18	69.2	206	27	US-60-412-418-2179	Sequence 2179, Ap
39	18	69.2	237	1	PCT-US01-14826-218	Sequence 218, Appl
40	18	69.2	237	13	PCT-US02-23913-91	Sequence 91, Appl
41	18	69.2	237	13	US-08-933-750-32	Sequence 32, Appl
42	18	69.2	237	12	US-09-818-865-32	Sequence 32, Appl
43	18	69.2	237	22	US-09-840-787-32	Sequence 32, Appl
44	18	69.2	237	26	US-10-205-823-91	Sequence 91, Appl
45	18	69.2	247	8	US-08-467-152-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-60-360-039-12686
Sequence 12686, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360, 039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12686
LENGTH: 310
TYPE: PRT
ORGANISM: Aspergillus nidulans
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(310)
OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-12686

Query Match 73.1% Score 19; DB 27; Length 310;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0;

QY 1 KXXXXXXXXD 10
DB 73 KKTAAAFALD 82

RESULT 2

US-09-733-089-16924
Sequence 16924, Application US/09733089
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovacic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/733,089
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/474,435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 16924
LENGTH: 358
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-733-089-16924

Query Match 73.1%; Score 19; DB 21; Length 358;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXD 10
DB 42 KKAADAAALD 51

RESULT 3

US-09-816-660-16924
Sequence 16924, Application US/09816660
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovacic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/816,660
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/474,435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/733,089
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER:)
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 16924
LENGTH: 358
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-816-660-16924

QY 1 KXXXXXXXXD 10
DB 42 KKAADAAALD 51

Query Match 73.1%; Score 19; DB 22; Length 358;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXD 10
DB 42 KKAADAAALD 51

RESULT 4

US-09-513-996A-43459
Sequence 43459, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 43459
LENGTH: 378
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: UNSURE
LOCATION: 1..378
OTHER INFORMATION: any n or Xaa = unknown
FEATURE:
OTHER INFORMATION: Location 1..378 / Ceres Seq. ID 1985639
US-09-513-996A-43459

Query Match 73.1%; Score 19; DB 19; Length 378;
Best Local Similarity 40.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXD 10
DB 13 KKAADAAALD 22

RESULT 5

US-09-708-427-18784
Sequence 18784, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18784
LENGTH: 378
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..378
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc. feature
LOCATION: 1..378
OTHER INFORMATION: Ceres Seq. ID 1834815
US-09-708-427-18784

Query Match 73.1%; Score 19; DB 21; Length 378;
Best Local Similarity 40.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXD 10
DB 13 KKAADAAALD 22

Db 13 KKAADAAALD 22

RESULT 6

US-09-791-537-114720

; Sequence 114720, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: Patent version 3.0

; SEQ ID NO 114720

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-791-537-114720

Query Match

Best Local Similarity 73.1%; Score 19; DB 21; Length 378;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

Db 13 KKAADAAALD 22

RESULT 7

US-60-356-051-2815

; Sequence 2815, Application US/60356051

; GENERAL INFORMATION:

; APPLICANT: Monsanto Technology LLC

; APPLICANT: Luffiyya, Linda L

; TITLE OF INVENTION: NUCLEIC ACIDS AND OTHER MOLECULES ASSOCIATED WITH

; FILE REFERENCE: 38-21 (15300)I

; CURRENT APPLICATION NUMBER: US/60/356,051

; CURRENT FILING DATE: 2002-02-11

; NUMBER OF SEQ ID NOS: 2926

; SOFTWARE: Patent version 3.1

; SEQ ID NO 2815

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-60-356-051-2815

Query Match

Best Local Similarity 73.1%; Score 19; DB 27; Length 378;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

Db 13 KKAADAAALD 22

RESULT 8

US-10-221-279-10068

; Sequence 10068, Application US/10221279

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

; FILE REFERENCE: 21272-046

; CURRENT APPLICATION NUMBER: US/10/221,279

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 09/574,454

; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: 09/519,705

; PRIOR FILING DATE: 2000-03-07

; NUMBER OF SEQ ID NOS: 12360

; SOFTWARE: Custom

; SEQ ID NO 10068

; LENGTH: 35

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-221-279-10068

Query Match

Best Local Similarity 69.2%; Score 18; DB 26; Length 35;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

Db 3 KKYSSQTSLD 12

RESULT 9

PCT-US99-22853B-42

; Sequence 42, Application PC/TUS9922853B

; GENERAL INFORMATION:

; APPLICANT: Ceres, Inc.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding

; FILE REFERENCE: 2750-0569f(PC)

; CURRENT APPLICATION NUMBER: PCT/US99/22853B

; CURRENT FILING DATE: 1999-10-05

; NUMBER OF SEQ ID NOS: 3938

; SOFTWARE: MS Word 97

; SEQ ID NO 42

; LENGTH: 43

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: LOCATION 1..43, Ceres Seq. ID 1685642

; NAME/KEY: UNSURE

; LOCATION: (1)..(43)

; OTHER INFORMATION: any Xaa - any amino acid, unknown or other

PCT-US99-22853B-42

Query Match

Best Local Similarity 69.2%; Score 18; DB 1; Length 43;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKKXXXXXLD 10

Db 5 KKLTTDALD 14

RESULT 10

PCT-US00-07527-111

; Sequence 111, Application PC/TUS0007527

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: 47 Human Secreted Proteins

; FILE REFERENCE: P5529PCT

; CURRENT APPLICATION NUMBER: PCT/US00/07527

; CURRENT FILING DATE: 2000-03-22

; EARLIER APPLICATION NUMBER: 60/126,600

; EARLIER FILING DATE: 1999-03-26

; EARLIER APPLICATION NUMBER: 60/171,550

; EARLIER FILING DATE: 1999-171,550

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: Patent Ver. 2.0

; SEQ ID NO 111

; LENGTH: 46

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-07527-111

Query Match

Best Local Similarity 69.2%; Score 18; DB 1; Length 46;

Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXX 10
DB 19 KKSAAESMLD 28

RESULT 11
PCT-US00-07527-112
; Sequence 112, Application PC/TUS0007527
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 47 Human Secreted Proteins
; FILE REFERENCE: PS529PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07527
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/126,600
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/171,550
; EARLIER FILING DATE: 1999-171,550
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07527-112

Query Match 69.2%; Score 18; DB 1; Length 46;
Best Local Similarity 40.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXX 10
DB 19 KKSAAESMLD 28

RESULT 12
PCT-US99-22853B-41
; Sequence 41, Application PC/TUS9922853B
; GENERAL INFORMATION:
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-0369F(PC)
; CURRENT APPLICATION NUMBER: PCT/US99/22853B
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 3938
; SOFTWARE: MS Word 97
; SEQ ID NO 41
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: LOCATION 1..54, Ceres Seq. ID 1685641
; OTHER INFORMATION: any Xaa - any amino acid, unknown or other
PCT-US99-22853B-41

Query Match 69.2%; Score 18; DB 1; Length 54;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXX 10
DB 16 KKLTTTDAID 25

RESULT 13
PCT-US99-22853B-40
; Sequence 40, Application PC/TUS9922853B
; GENERAL INFORMATION:
; APPLICANT: Ceres, Inc.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-0569F(PC)
; CURRENT APPLICATION NUMBER: PCT/US99/22853B
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 3938
; SOFTWARE: MS Word 97
; SEQ ID NO 40
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: LOCATION 1..79, Ceres Seq. ID 1685640
; NAME/KEY: UNSURE
; LOCATION: (1)..(79)
; OTHER INFORMATION: any Xaa - any amino acid, unknown or other
PCT-US99-22853B-40

Query Match 69.2%; Score 18; DB 1; Length 79;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXX 10
DB 41 KKLTTTDAID 50

RESULT 14
US-09-134-000-5378
; Sequence 5378, Application US/09134000A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucelte-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
; FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134,000A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 5378
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000-5378

Query Match 69.2%; Score 18; DB 15; Length 87;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXX 10
DB 44 KKSRAFAASLD 53

RESULT 15
US-09-758-472-8508
; Sequence 8508, Application US/09758472
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PH001
; CURRENT APPLICATION NUMBER: US/09/758,472
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9632
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8508
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-472-8508

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Query Match      69.2%; Score 18; DB 21; Length 89;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      1 KKKXXXXXD 10
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DB      43 KKAISALD 52

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Search completed: June 5, 2003, 15:47:36
 Job time : 125.182 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 5, 2003, 15:31:47 ; Search time 28.4848 Seconds
(without alignments)
74.544 Million cell updates/sec

Title: US-09-150-947F-14
Perfect score: 26
Sequence: 1 KKKXXXXXLD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1012620 seqs, 212337834 residues

Total number of hits satisfying chosen parameters: 1012620

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	73.1	310	6	US-10-369-493-12686 Sequence 12686, A
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4	18	69.2	87	5	US-09-134-000C-5378 Sequence 5378, Ap
5	18	69.2	100	6	US-10-421-684-1170 Sequence 1170, Ap
6	18	69.2	109	5	US-09-724-676-55061 Sequence 55061, A
7	18	69.2	109	5	US-09-724-676-55061 Sequence 55061, A
8	18	69.2	147	5	US-09-513-999C-6288 Sequence 6288, Ap
9	18	69.2	147	5	US-09-513-999C-6288 Sequence 6288, Ap
10	18	69.2	152	5	US-09-949-016-6460 Sequence 6460, App
11	18	69.2	152	7	US-60-440-068-114 Sequence 114, App
12	18	69.2	161	5	US-09-724-676-55060 Sequence 55060, A
13	18	69.2	161	5	US-09-724-676-55060 Sequence 55060, A
14	18	69.2	252	6	US-10-282-122A-52371 Sequence 52371, A
15	18	69.2	254	6	US-10-431-652-7651 Sequence 7651, Ap
16	18	69.2	315	6	US-10-431-652-4290 Sequence 4290, Ap
17	18	69.2	318	6	US-10-272-490-90 Sequence 90, Appl
18	18	69.2	318	6	US-10-272-490-90 Sequence 90, Appl
19	18	69.2	328	6	US-10-363-616-281 Sequence 281, Appl
20	18	69.2	341	6	US-10-272-490-68 Sequence 68, Appl
21	18	69.2	341	6	US-10-272-490-68 Sequence 68, Appl
22	18	69.2	341	6	US-10-214-473-68 Sequence 68, Appl
23	18	69.2	341	6	US-10-214-473-68 Sequence 68, Appl
24	18	69.2	406	6	US-10-425-114-70484 Sequence 70484, A
25	18	69.2	768	6	US-10-218-140-4424 Sequence 4424, A
26	18	69.2	837	6	US-10-369-493-22296 Sequence 22296, A

27	17	65.4	12	6	US-10-172-425B-53	Sequence 53, Appl
28	17	65.4	14	6	US-10-172-425B-37	Sequence 37, Appl
29	17	65.4	14	6	US-10-172-425B-49	Sequence 49, Appl
30	17	65.4	53	6	US-10-424-599-172337	Sequence 172337, Ap
31	17	65.4	57	6	US-10-424-599-172320	Sequence 172320, Ap
32	17	65.4	70	6	US-10-424-599-233335	Sequence 233335, Ap
33	17	65.4	77	6	US-10-424-599-225608	Sequence 225608, Ap
34	17	65.4	85	6	US-10-424-599-194596	Sequence 194596, Ap
35	17	65.4	106	6	US-09-864-408A-3042	Sequence 3042, Ap
36	17	65.4	109	6	US-10-424-599-167306	Sequence 167306, Ap
37	17	65.4	128	6	US-10-357-886-44	Sequence 44, Appl
38	17	65.4	142	5	US-09-857-826B-18	Sequence 18, Appl
39	17	65.4	143	6	US-10-276-774-2588	Sequence 2588, Ap
40	17	65.4	152	6	US-10-417-884-3744	Sequence 3744, Ap
41	17	65.4	160	6	US-10-424-599-170060	Sequence 170060, Ap
42	17	65.4	170	6	US-10-264-237-2676	Sequence 2676, Ap
43	17	65.4	178	6	US-10-282-122A-44631	Sequence 44631, A
44	17	65.4	189	6	US-10-094-749-2347	Sequence 2347, Ap
45	17	65.4	192	5	US-09-675-784A-8051	Sequence 8051, Ap

ALIGNMENTS

RESULT 1
US-10-369-493-12686
Sequence 12686, Application US/10369493
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
CURRENT FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12686
LENGTH: 310
TYPE: PRT
ORGANISM: Aspergillus nidulans
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(310)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12686

Query Match
Best Local Similarity 73.18; Score 19; DB 6; Length 310;
Matches 4; Conservative 0; Pred. No. 1.7e+02; Indels 6; Gaps 0;
Matches 4; Conservative 0; Pred. No. 1.7e+02; Indels 6; Gaps 0;

DB 73 KKTAAFD 82
1 KKKXXXXXLD 10

RESULT 2
US-10-361-942-986
Sequence 986, Application US/10361942
GENERAL INFORMATION:
APPLICANT: Lufiyya, Linda L.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)K
CURRENT APPLICATION NUMBER: US/10/361,942
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/356,051
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 2906

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;; SEQ ID NO 986
;; LENGTH: 378
;; TYPE: PRT
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;;   OTHER INFORMATION: Clone ID: AT_T6A23.C1.p24.tg
US-10-361-942-986
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Query Match          73.1%; Score 19; DB 6; Length 378;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 1 KKKXXXXXLD 10
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DB 13 KKADAAALD 22
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RESULT 3
US-09-134-000C-5378
; Sequence 5378, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5378
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5378
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Query Match          69.2%; Score 18; DB 5; Length 87;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 1 KKKXXXXXLD 10
    ||
DB 44 KKSRAFASLD 53
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```
RESULT 4
US-09-134-000C-5378
; Sequence 5378, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5378
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5378
```

```
Query Match          69.2%; Score 18; DB 5; Length 87;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 1 KKKXXXXXLD 10
    ||
DB 44 KKSRAFASLD 53
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RESULT 5
US-10-421-684-1170
; Sequence 1170, Application US/10421684
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
```

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; APPLICANT: Liang, Jihong
; APPLICANT: Miltanek, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
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; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
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; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/10/421,684
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; CURRENT FILING DATE: 2003-04-23
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; PRIOR APPLICATION NUMBER: US/09/732,210
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; PRIOR FILING DATE: 2000-12-07
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; PRIOR APPLICATION NUMBER: US 60/169,513
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; PRIOR FILING DATE: 1999-12-07
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; PRIOR APPLICATION NUMBER: US 60/169,340
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; PRIOR FILING DATE: 1999-12-07
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; NUMBER OF SEQ ID NOS: 1753
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; SEQ ID NO 1170
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Marchantia polymorpha
US-10-421-684-1170
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Query Match          69.2%; Score 18; DB 6; Length 100;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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OY 1 KKKXXXXXLD 10
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DB 29 KRIETSSLD 38
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RESULT 6
US-09-724-676-55061
; Sequence 55061, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55061
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-55061
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Query Match          69.2%; Score 18; DB 5; Length 109;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 1 KKKXXXXXLD 10
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DB 44 KKSAAESMLD 53
```

```
RESULT 7
US-09-724-676A-55061
; Sequence 55061, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 55061
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-55061

Query Match 69.2%; Score 18; DB 5; Length 109;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXLD 10
DB 44 KKSAAESMLD 53

RESULT 8
US-09-513-999C-6288
Sequence 6288, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Duclert, A. Y.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.052.NEG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6288
LENGTH: 147
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6288

Query Match 69.2%; Score 18; DB 5; Length 147;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXLD 10
DB 78 KKKRAATYLD 87

RESULT 9
US-09-513-999C-6288
Sequence 6288, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Duclert, A. Y.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.052.NEG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6288
LENGTH: 147
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6288

Query Match 69.2%; Score 18; DB 5; Length 147;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 78 KKKRAATYLD 87

RESULT 10
US-09-949-016-6460
Sequence 6460, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6460
LENGTH: 152
TYPE: PRT
ORGANISM: Human
US-09-949-016-6460

Query Match 69.2%; Score 18; DB 5; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXLD 10
DB 44 KKSAAESMLD 53

RESULT 11
US-60-440-068-114
Sequence 114, Application US/60440068
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
TITLE OF INVENTION: NF-KB PATHWAY
FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440.068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 114
LENGTH: 152
TYPE: PRT
ORGANISM: Homo sapiens
US-60-440-068-114

Query Match 69.2%; Score 18; DB 7; Length 152;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 KXXXXXXXXLD 10
DB 44 KKSAAESMLD 53

RESULT 12
US-09-724-676-55060
Sequence 55060, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Comugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Comugen
CURRENT APPLICATION NUMBER: US/09/724.676
CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55060
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-55060

Query Match 69.2% Score 18; DB 5; Length 161;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXXXXD 10
DB 44 KKSAAESMLD 53

RESULT 13

US-09-724-676A-55060
Sequence 55060, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55060
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-55060

Query Match 69.2% Score 18; DB 5; Length 161;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXXXXD 10
DB 44 KKSAAESMLD 53

RESULT 14

US-10-282-122A-52371
Sequence 52371, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.03A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52371
LENGTH: 252
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52371

Query Match 69.2% Score 18; DB 6; Length 252;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXXXXD 10
DB 9 KRASTDTNLD 18

RESULT 15

US-10-431-652-7651
Sequence 7651, Application US/10431652
GENERAL INFORMATION:
APPLICANT: Breton, Gary L.
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
FILE REFERENCE: PAT03-08
CURRENT APPLICATION NUMBER: US/10/431,652
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 09/328,352
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,701
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7651
LENGTH: 254
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-10-431-652-7651

Query Match 69.2% Score 18; DB 6; Length 254;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 KXXXXXXXXXD 10
DB 210 KRSGSKTLD 219

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Job time: 33.4848 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:29:17 ; Search time 123.182 Seconds

(without alignments)
52.340 Million cell updates/sec

Title: US-09-150-947f-15

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	40.0	2	1	PCT-US00-00358-13
2	6	40.0	2	1	PCT-US00-08879-16
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5	6	40.0	2	1	PCT-US00-08879A-16
6	6	40.0	2	1	PCT-US00-08879A-18

7	6	40.0	2	1	PCT-US00-08879A-30	Sequence 30, App1
8	6	40.0	2	1	PCT-US02-09188-532	Sequence 532, App
9	6	40.0	2	1	PCT-US02-09239-152	Sequence 152, App
10	6	40.0	2	1	PCT-US02-09370-551	Sequence 551, App
11	6	40.0	2	1	PCT-US02-23763-296	Sequence 296, App
12	6	40.0	2	1	PCT-US02-30452-85	Sequence 85, App1
13	6	40.0	2	1	PCT-US99-26100-6	Sequence 6, App11
14	6	40.0	2	3	US-07-853-042A-3	Sequence 3, App11
15	6	40.0	2	6	US-08-222-626A-122	Sequence 122, App
16	6	40.0	2	6	US-08-248-816-8	Sequence 8, App11
17	6	40.0	2	8	US-08-430-121-8	Sequence 8, App11
18	6	40.0	2	8	US-08-472-679B-15	Sequence 15, App1
19	6	40.0	2	8	US-08-472-679B-23	Sequence 23, App1
20	6	40.0	2	8	US-08-472-679B-33	Sequence 33, App1
21	6	40.0	2	8	US-08-472-679B-39	Sequence 39, App1
22	6	40.0	2	8	US-08-472-679D-15	Sequence 15, App1
23	6	40.0	2	8	US-08-472-679D-23	Sequence 23, App1
24	6	40.0	2	8	US-08-472-679D-33	Sequence 33, App1
25	6	40.0	2	8	US-08-472-679D-39	Sequence 39, App1
26	6	40.0	2	8	US-08-472-679H-15	Sequence 15, App1
27	6	40.0	2	8	US-08-472-679H-23	Sequence 23, App1
28	6	40.0	2	8	US-08-472-679H-33	Sequence 33, App1
29	6	40.0	2	8	US-08-472-679H-39	Sequence 39, App1
30	6	40.0	2	10	US-08-633-879B-85	Sequence 85, App1
31	6	40.0	2	11	US-08-783-79B-85	Sequence 85, App1
32	6	40.0	2	12	US-08-843-675A-72	Sequence 72, App1
33	6	40.0	2	16	US-09-295-846-24	Sequence 24, App1
34	6	40.0	2	16	US-09-295-846-26	Sequence 26, App1
35	6	40.0	2	16	US-09-295-846-38	Sequence 38, App1
36	6	40.0	2	16	US-09-295-846A-24	Sequence 24, App1
37	6	40.0	2	16	US-09-295-846A-26	Sequence 26, App1
38	6	40.0	2	16	US-09-295-846A-38	Sequence 38, App1
39	6	40.0	2	16	US-09-295-846B-24	Sequence 24, App1
40	6	40.0	2	16	US-09-295-846B-26	Sequence 26, App1
41	6	40.0	2	16	US-09-295-846B-38	Sequence 38, App1
42	6	40.0	2	16	US-09-295-924B-18	Sequence 18, App1
43	6	40.0	2	16	US-09-295-924B-20	Sequence 20, App1
44	6	40.0	2	16	US-09-295-924B-32	Sequence 32, App1
45	6	40.0	2	16	US-09-296-113A-21	Sequence 21, App1

ALIGNMENTS

RESULT 1
PCT-US00-00358-13
Sequence 13, Application PC/TUS0000358
GENERAL INFORMATION:
APPLICANT: pecker, Iris
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY DISTANTLY HOW
FILE REFERENCE: 00/20105
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/140,801
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-00358-13

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 D 10
Db 1 D 1

RESULT 2
PCT-US00-08879-16
; Sequence 16, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 16
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-16

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 3
PCT-US00-08879-18
; Sequence 18, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-18

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 4
PCT-US00-08879-30
; Sequence 30, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT

; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-30

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 2 D 2

RESULT 5
PCT-US00-08879A-16
; Sequence 16, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 16
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-16

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 6
PCT-US00-08879A-18
; Sequence 18, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-18

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 7
PCT-US00-08879A-30

; Sequence 30, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-30

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 2 D 2

RESULT 8
PCT-US02-09188-532

; Sequence 532, Application PC/TUS0209188
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS952PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09188
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1732
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 532
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09188-532

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 9

PCT-US02-09239-152
; Sequence 152, Application PC/TUS0209239
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS953PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09239
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09239-152

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 10
PCT-US02-09370-551

; Sequence 551, Application PC/TUS0209370
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS954PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09370
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1834
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 551
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09370-551

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 11
PCT-US02-23763-296

; Sequence 296, Application PC/TUS0223763
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: PCT/US02/23763
; CURRENT FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: US 60/308,523
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/351,289
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/366,854
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 60/385,362
PRIOR FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 307
SOFTWARE: PatentIn version 3.1
SEQ ID NO 296
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-23763-296

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 2 D 2

RESULT 12
PCT-US02-30452-85
Sequence 85, Application PC/TUS0230452
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
FILE REFERENCE: 08702.00012-00304
CURRENT APPLICATION NUMBER: PCT/US02/30452
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: 60/334,528
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-30452-85

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 2 D 2

RESULT 13
PCT-US99-26100-6
Sequence 6, Application PC/TUS9926100
GENERAL INFORMATION:
APPLICANT: Ream, Walt et al.,
TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
TITLE OF INVENTION: Methods and Compositions for Producing the Same
FILE REFERENCE: 53629
CURRENT APPLICATION NUMBER: PCT/US99/26100
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: 60/107,185
EARLIER FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 2
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
PCT-US99-26100-6

Query Match 40.0%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 2 D 2

RESULT 14
US-07-853-042A-3
Sequence 3, Application US/07853042A
GENERAL INFORMATION:
APPLICANT: Anders BIL
TITLE OF INVENTION: METHOD AND MEANS FOR INDUCING, RESP.,
TITLE OF INVENTION: PREVENTING CONSTRICTION OF THE PUPIL
TITLE OF INVENTION: IN THE EYE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FRED PHILPITT
STREET: 99 Canal Center Plaza, Ste. 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,042A
FILING DATE: 19920318
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FRED PHILPITT
REGISTRATION NUMBER: 16825
REFERENCE/DOCKET NUMBER: PHE-808
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide

US-07-853-042A-3

Query Match 40.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
Db 1 D 1

RESULT 15
US-08-222-626A-122
Sequence 122, Application US/08222626A
GENERAL INFORMATION:
APPLICANT: Aral, Naoko
APPLICANT: Masuda, Esteban S.
APPLICANT: Tokumitsu, Hiroshi
TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California

COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,626A
FILING DATE: 04-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,061
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113,971
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,998
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,483
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0392K3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEX: 415-496-1200
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-222-626A-122

Query Match 40.0%; Score 6; DB 6; Length 2;

Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 D 10
Db 1 D 1

Search completed: June 5, 2003, 15:47:37
Job time : 124.182 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:47 ; Search time 28.4848 seconds
(without alignments)
74.544 Million cell updates/sec

Title: US-09-150-947f-15
Perfect score: 15
Sequence: 1 xxxxxxxxxx 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1012620 seqs, 212337834 residues

Total number of hits satisfying chosen parameters: 1012620

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/prodata/1/paa/pct_US07_NEW_COMB.pep:*
4: /cgn2_6/prodata/1/paa/pct_US08_NEW_COMB.pep:*
5: /cgn2_6/prodata/1/paa/pct_US09_NEW_COMB.pep:*
6: /cgn2_6/prodata/1/paa/pct_US10_NEW_COMB.pep:*
7: /cgn2_6/prodata/1/paa/pct_US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	2	4	US-08-472-679H-15
2	6	40.0	2	4	US-08-472-679H-23
3	6	40.0	2	4	US-08-472-679H-33
4	6	40.0	2	4	US-08-472-679H-39
5	6	40.0	2	4	US-08-472-679H-15
6	6	40.0	2	4	US-08-472-679H-23
7	6	40.0	2	4	US-08-472-679H-33
8	6	40.0	2	4	US-08-472-679H-39
9	6	40.0	2	6	US-10-109-048-461
10	6	40.0	2	6	US-10-109-048-461
11	6	40.0	2	6	US-10-405-027-5115
12	6	40.0	3	1	PCT-US02-14358-15
13	6	40.0	3	1	PCT-US02-14358-16
14	6	40.0	3	1	PCT-US02-14358-17
15	6	40.0	3	1	PCT-US02-14358-18
16	6	40.0	3	1	PCT-US02-14358-19
17	6	40.0	3	1	PCT-US02-14358-20
18	6	40.0	3	1	PCT-US02-21322-6
19	6	40.0	3	1	PCT-US02-21322A-6
20	6	40.0	3	1	PCT-US02-26918A-316
21	6	40.0	3	1	PCT-US02-26918A-317
22	6	40.0	3	1	PCT-US02-26918A-318
23	6	40.0	3	1	PCT-US02-26918A-319
24	6	40.0	3	1	PCT-US03-00079-30
25	6	40.0	3	1	PCT-US03-10473-6
26	6	40.0	3	1	PCT-US03-11798-8

27	6	40.0	3	1	PCT-US03-14096-24	Sequence 24, Appl
28	6	40.0	3	5	US-09-302-195C-1	Sequence 1, Appl
29	6	40.0	3	5	US-09-716-394-11	Sequence 11, Appl
30	6	40.0	3	5	US-09-853-080A-37	Sequence 37, Appl
31	6	40.0	3	5	US-09-772-819-11	Sequence 11, Appl
32	6	40.0	3	5	US-09-573-830-11	Sequence 11, Appl
33	6	40.0	3	5	US-09-992-124B-74	Sequence 74, Appl
34	6	40.0	3	5	US-09-564-045-11	Sequence 11, Appl
35	6	40.0	3	5	US-09-867-847A-30	Sequence 30, Appl
36	6	40.0	3	5	US-09-980-347-6	Sequence 6, Appl
37	6	40.0	3	5	US-09-723-437B-11	Sequence 11, Appl
38	6	40.0	3	5	US-09-939-481-81	Sequence 81, Appl
39	6	40.0	3	5	US-09-898-165B-33	Sequence 33, Appl
40	6	40.0	3	5	US-09-623-548A-1053	Sequence 1053, Ap
41	6	40.0	3	5	US-09-623-548A-1054	Sequence 1054, Ap
42	6	40.0	3	5	US-09-623-548A-1160	Sequence 1160, Ap
43	6	40.0	3	5	US-09-623-548A-1170	Sequence 1170, Ap
44	6	40.0	3	6	US-10-141-531-15	Sequence 15, Appl
45	6	40.0	3	6	US-10-141-531-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-472-679H-15
; Sequence 15, Application US/08472679H
GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.
Junker, David E.

TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

LENGTH: 2 amino acids

TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-472-679H-15

Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 D 10
Db 1 D 1

RESULT 2

US-08-472-679H-23
; Sequence 23, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-472-679H-23
Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 D 10
DB 1 D 1
RESULT 3
US-08-472-679H-33
; Sequence 33, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33
Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 D 10
DB 1 D 1
RESULT 4
US-08-472-679H-39
; Sequence 39, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-08-472-679H-39
Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 D 10
DB 1 D 1
RESULT 5
US-08-472-679H-15
; Sequence 15, Application US/08472679H

US-08-472-679H-33
; Sequence 33, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33
Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 D 10
DB 1 D 1
RESULT 4
US-08-472-679H-39
; Sequence 39, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-08-472-679H-39
Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 D 10
DB 1 D 1
RESULT 5
US-08-472-679H-15
; Sequence 15, Application US/08472679H

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/472,679H
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-472-679H-15

Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
DB 1 D 1

RESULT 6
US-08-472-679H-23
Sequence 23, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/472,679H
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33

TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-472-679H-23

Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
DB 1 D 1

RESULT 7
US-08-472-679H-33
Sequence 33, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/472,679H
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33

Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 D 10
DB 1 D 1

RESULT 8
US-08-472-679H-39
Sequence 39, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.

Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeid
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeid, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-08-472-679H-39

Query Match 40.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 9
US-10-187-339-6
Sequence 6, Application US/10187339
GENERAL INFORMATION:
APPLICANT: Ream, Walt et al.
TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
FILE REFERENCE: 53629
CURRENT APPLICATION NUMBER: US/10/187,339
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/434,837
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,185
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 2
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-187-339-6

Query Match 40.0%; Score 6; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 2 D 2

RESULT 10
US-10-109-048-461
Sequence 461, Application US/10109048
GENERAL INFORMATION:
APPLICANT: COMMORI, PADMA
APPLICANT: KEELING, PETER L.
APPLICANT: RAMIREZ, NONA
APPLICANT: MCKEAN, ANGELA
APPLICANT: GAO, ZHONG
APPLICANT: GUAN, HANPING
TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
FILE REFERENCE: 2461-76
CURRENT APPLICATION NUMBER: US/10/109,048
CURRENT FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/279,720
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 1154
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 461
LENGTH: 2
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Accession No. 3832512
US-10-109-048-461

Query Match 40.0%; Score 6; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 2 D 2

RESULT 11
US-10-405-027-5115
Sequence 5115, Application US/10405027
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS806P1
CURRENT APPLICATION NUMBER: US/10/405,027
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/369,608
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/376,175
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 5810
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5115
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
US-10-405-027-5115

Query Match 40.0%; Score 6; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
DB 1 D 1

RESULT 12
PCT-US02-14358-15
Sequence 15, Application PC/TUS0214358
GENERAL INFORMATION:
APPLICANT: XENCOR
APPLICANT: SINGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.

APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Lugnbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 3
TYPE: PRT
ORGANISM: Escherichia coli
PCT-US02-14358-15

Query Match 40.0%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 13
PCT-US02-14358-16
Sequence 16, Application PC/TUS0214358
GENERAL INFORMATION:
APPLICANT: XENCOR
APPLICANT: SYNGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Lugnbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 3
TYPE: PRT
ORGANISM: Bacillus subtilis
PCT-US02-14358-16

Query Match 40.0%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 14
PCT-US02-14358-17
Sequence 17, Application PC/TUS0214358
GENERAL INFORMATION:

APPLICANT: XENCOR
APPLICANT: SYNGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Lugnbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 3
TYPE: PRT
ORGANISM: Mycobacterium leprae
PCT-US02-14358-17

Query Match 40.0%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

RESULT 15
PCT-US02-14358-18
Sequence 18, Application PC/TUS0214358
GENERAL INFORMATION:
APPLICANT: XENCOR
APPLICANT: SYNGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Lugnbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 3
TYPE: PRT
ORGANISM: Sarccharomyces cerevisiae
PCT-US02-14358-18

Query Match 40.0%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 D 10
|
Db 1 D 1

Search completed: June 5, 2003, 15:52:27

Fri Jun 6 09:14:41 2003

us-09-150-947f-15.rapn

Page 6

Job time : 29.4848 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:29:17 ; Search time 147.818 Seconds

(Without alignments)
52,340 Million cell updates/sec

Title: US-09-150-947F-16

Perfect score: 33

Sequence: 1 XXXXXXTXQEXD 12

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Searched: 4569144 seqs, 64473110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Pending_Patents_AA_Main:*

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*

3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	24	72.7	209	21	US-09-791-537-103704
6	24	72.7	209	21	US-09-791-537-103705

7	24	72.7	209	21	US-09-791-537-103706
8	24	72.7	209	21	US-09-791-537-103708
9	24	72.7	209	21	US-09-791-537-103712
10	24	72.7	209	21	US-09-791-537-103715
11	24	72.7	209	21	US-09-791-537-103717
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13	24	72.7	209	21	US-09-791-537-103720
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15	24	72.7	209	21	US-09-791-537-103733
16	24	72.7	209	21	US-09-791-537-103736
17	24	72.7	209	21	US-09-791-537-103738
18	24	72.7	209	21	US-09-791-537-103740
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21	24	72.7	209	21	US-09-791-537-137418
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ALIGNMENTS

US-09-869-136-9

Sequence 9, Application US/09869136

GENERAL INFORMATION:

APPLICANT: FRASER, JOHN DAVID

APPLICANT: PROF, THOMAS

TITLE OF INVENTION: SUPERANTIGENS

FILE REFERENCE: 3911-8

CURRENT APPLICATION NUMBER: US/09/869,136

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: PCT/NZ99/00228

PRIOR FILING DATE: 1999-12-24

PRIOR APPLICATION NUMBER: NZ 333589

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentlin Ver. 2.1

SEQ ID NO 9

LENGTH: 204

TYPE: PRT

ORGANISM: Streptococcus pyogenes

US-09-869-136-9

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; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103693
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103693

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Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 3
US-09-791-537-103695
; Sequence 103695, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103695
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103695

Query Match
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Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
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; Sequence 103701, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; SOFTWARE: PatentIn version 3.0
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; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103701

Query Match
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Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 125 KTVTAQAEID 134

RESULT 5
US-09-791-537-103704
; Sequence 103704, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103704

Query Match
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QY 3 KXXXTXQEXD 12
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Db 125 KTVTAQAEID 134

RESULT 6
US-09-791-537-103705
; Sequence 103705, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
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; SOFTWARE: PatentIn version 3.0
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103705

Query Match
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Pred. No. 6.1e+02;
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QY 3 KXXXTXQEXD 12
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RESULT 7
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; Sequence 103706, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; TYPE: PRF
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103706

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RESULT 8
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; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; TYPE: PRF
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103708

Query Match
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; Sequence 103712, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
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US-09-791-537-103712

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DB 125 KTTVTAQXEND 134

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; Sequence 103715, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
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; ORGANISM: Streptococcus pyogenes
US-09-791-537-103715

Query Match
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DB 125 KTTVTAQXEND 134

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; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 209
; TYPE: PRF
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103717

Query Match
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OY 3 KXXXTXQXEND 12
DB 125 KTTVTAQXEND 134

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RESULT 12
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; Sequence 103719, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBR
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103719
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103719

Query Match
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Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 125 KTYVTAQCID 134

RESULT 13
US-09-791-537-103720
; Sequence 103720, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBR
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103720
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103720

Query Match
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Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 125 KTYVTAQCID 134

RESULT 14
US-09-791-537-103729
; Sequence 103729, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBR
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103729
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103729

Query Match
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Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 125 KTYVTAQCID 134

RESULT 15
US-09-791-537-103733
; Sequence 103733, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103733
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-791-537-103733

Query Match
Best Local Similarity 72.7%; Score 24; DB 21; Length 209;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTXQEXD 12
DB 125 KTYVTAQCID 134
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Search completed: June 5, 2003, 15:47:37
Job time : 147.818 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:47 ; Search time 34.1818 Seconds
(without alignments)
74.544 Million cell updates/sec

Title: US-09-150-947F-16
Perfect score: 33
Sequence: 1 XXXXXXTXQEXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1012620 seqs, 212337834 residues
Total number of hits satisfying chosen parameters: 1012620

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	24	72.7	278	5	US-09-675-784A-11175 Sequence 11175, A
3	23	69.7	14	6	US-10-172-425B-37 Sequence 37, Appl
4	23	69.7	115	5	US-09-134-000C-6190 Sequence 6190, Ap
5	23	69.7	115	5	US-09-134-000C-6190 Sequence 6190, Ap
6	23	69.7	134	6	US-10-424-599-184221 Sequence 184221, Ap
7	23	69.7	228	6	US-10-203-536-1 Sequence 1, Appl1
8	23	69.7	266	5	US-09-751-708A-12 Sequence 12, Appl
9	23	69.7	281	6	US-10-424-599-179861 Sequence 179861, Ap
10	23	69.7	324	7	US-60-440-068-124 Sequence 1205, Ap
11	23	69.7	627	6	US-10-431-652-7705 Sequence 7705, Ap
12	22	66.7	10	5	US-09-150-947F-3 Sequence 3, Appl1
13	22	66.7	10	5	US-09-150-947F-4 Sequence 4, Appl1
14	22	66.7	10	6	US-10-172-425B-3 Sequence 3, Appl1
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18	22	66.7	12	6	US-10-172-425B-1 Sequence 1, Appl1
19	22	66.7	12	6	US-10-172-425B-2 Sequence 2, Appl1
20	22	66.7	12	6	US-10-172-425B-52 Sequence 52, Appl
21	22	66.7	12	7	US-60-458-305-26 Sequence 26, Appl
22	22	66.7	13	7	US-60-458-305-29 Sequence 29, Appl
23	22	66.7	13	5	US-09-150-947F-5 Sequence 5, Appl1
24	22	66.7	13	5	US-09-150-947F-6 Sequence 6, Appl1
25	22	66.7	13	5	US-09-150-947F-11 Sequence 11, Appl
26	22	66.7	13	6	US-10-172-425B-5 Sequence 5, Appl1

27	22	66.7	13	6	US-10-172-425B-6 Sequence 6, Appl1
28	22	66.7	13	6	US-10-172-425B-11 Sequence 11, Appl
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34	22	66.7	14	6	US-10-172-425B-15 Sequence 15, Appl
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42	22	66.7	14	6	US-10-172-425B-47 Sequence 47, Appl
43	22	66.7	14	6	US-10-172-425B-50 Sequence 50, Appl
44	22	66.7	16	6	US-10-172-425B-14 Sequence 14, Appl
45	22	66.7	24	5	US-09-150-947F-7 Sequence 7, Appl1

ALIGNMENTS

```
RESULT 1
US-10-172-425B-33
; Sequence 33, Application US/10172425B
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGNIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-172-425B-33
Query Match. 72.7%; Score 24; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
CY 3 XXXXXXTXQEXD 12
DB 5 KTVTAQEDID 14
RESULT 2
US-09-675-784A-11175
; Sequence 11175, Application US/09675784A
; GENERAL INFORMATION:
; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIMER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORK
; APPLICANT: ZENG, QIANJONG
; APPLICANT: GREENE, JONATHAN R.
; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
; FILE REFERENCE: 2976-4020051
; CURRENT APPLICATION NUMBER: US/09/675,784A
```

;; CURRENT FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/156,338
;; PRIOR FILING DATE: 1999-09-29
;; NUMBER OF SEQ ID NOS: 13925
;; SEQ ID NO 11175
;; LENGTH: 278
;; TYPE: PRT
;; ORGANISM: Aspergillus fumigatus
US-09-675-784A-11175

Query Match 72.7%; Score 24; DB 5; Length 278;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTQXEND 12
| | | |
DB 126 KSDTTQDESD 135

RESULT 3
US-10-172-425B-37
; Sequence 37, Application US/10172425B
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-37

Query Match 69.7%; Score 23; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTQXEND 12
| | | |
DB 5 KRSVTAQELD 14

RESULT 4
US-09-134-000C-6190
; Sequence 6190, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6190
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6190

Query Match 69.7%; Score 23; DB 5; Length 115;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTQXEND 12
| | | |
DB 85 KKESTQXEVD 94

RESULT 5
US-09-134-000C-6190
; Sequence 6190, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6190
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6190

Query Match 69.7%; Score 23; DB 5; Length 115;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTQXEND 12
| | | |
DB 85 KKESTQXEVD 94

RESULT 6
US-10-424-599-184221
; Sequence 184221, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184221
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137368C.1.pcp
US-10-424-599-184221

Query Match 69.7%; Score 23; DB 6; Length 134;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXXXTQXEND 12
| | | |
DB 21 KTHDTSQELD 30

RESULT 7
US-10-203-536-1
; Sequence 1, Application US/10203536
; GENERAL INFORMATION:

APPLICANT: LEE, Hong-Kyun
APPLICANT: PARK, Yong-Ho
APPLICANT: HAN, Kyu-Boem
APPLICANT: CHANG, Byoung-Sun
APPLICANT: LEE, Yong-Jun
TITLE OF INVENTION: Staphylococcal Enterotoxin SEC-SER, Expression Vector and Host Cell
FILE REFERENCE: 0808-0329P
CURRENT APPLICATION NUMBER: US/10/203,536
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: PCT/KR00/01241
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: KR 2000-0007612
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 228
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Staphylococcal enterotoxin SEC-SER
US-10-203-536-1

Query Match 69.7%; Score 23; DB 6; Length 228;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQXND 12
DB 140 KKSXTAQEED 149

RESULT 8
US-09-751-708A-12
Sequence 12, Application US/09751708A
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match 69.7%; Score 23; DB 5; Length 266;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQXND 12
DB 178 KKSXTAQEED 187

RESULT 9
US-10-424-599-179861
Sequence 179861, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 179861
LENGTH: 281
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_13342C.1.pep
US-10-424-599-179861

Query Match 69.7%; Score 23; DB 6; Length 281;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQXND 12
DB 176 KKSXTAQEED 185

RESULT 10
US-60-440-068-124
Sequence 124, Application US/60440068
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGTH: 324
TYPE: PRT
ORGANISM: Homo sapiens
US-60-440-068-124

Query Match 69.7%; Score 23; DB 7; Length 324;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQXND 12
DB 193 KKSXTAQEED 202

RESULT 11
US-10-431-652-7705
Sequence 7705, Application US/10431652
GENERAL INFORMATION:
APPLICANT: Breton, Gary L.
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PAT03-08
CURRENT APPLICATION NUMBER: US/10/431,652
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 09/328,352
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 60/088,701
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7705
LENGTH: 627
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-10-431-652-7705

Query Match 69.7%; Score 23; DB 6; Length 627;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 Db 355 KSKVTAQELD 364

RESULT 12

US-09-150-947F-3
 ; Sequence 3, Application US/09150947F
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Arad, Gila
 ; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS ANTAGONISTS VACCINES
 ; FILE REFERENCE: A31967-PCT-USA-A 066031.0102
 ; CURRENT FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: PCT/IL97/00438
 ; PRIOR FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: ISRAEL 119938
 ; PRIOR FILING DATE: 1996-12-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-150-947F-3

Query Match 66.7%; Score 22; DB 5; Length 10;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 Db 1 KKKATVQELD 10

RESULT 13

US-09-150-947F-4
 ; Sequence 4, Application US/09150947F
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Arad, Gila
 ; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS ANTAGONISTS VACCINES
 ; FILE REFERENCE: A31967-PCT-USA-A 066031.0102
 ; CURRENT FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: PCT/IL97/00438
 ; PRIOR FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: ISRAEL 119938
 ; PRIOR FILING DATE: 1996-12-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-150-947F-4

Query Match 66.7%; Score 22; DB 5; Length 10;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 Db 1 KKKVTAQELD 10

RESULT 14

US-10-172-425B-3
 ; Sequence 3, Application US/10172425B
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Arad, Gila

;; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
 ;; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
 ;; CURRENT FILING DATE: 2002-06-13
 ;; PRIOR APPLICATION NUMBER: 09/150,947
 ;; PRIOR FILING DATE: 1998-09-10
 ;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
 ;; PRIOR FILING DATE: 1997-12-30
 ;; PRIOR APPLICATION NUMBER: ISRAEL 119938
 ;; PRIOR FILING DATE: 1996-12-30
 ;; NUMBER OF SEQ ID NOS: 57
 ;; SOFTWARE: FastSeq for Windows Version 4.0
 ;; SEQ ID NO 3
 ;; LENGTH: 10
 ;; TYPE: PRT
 ;; ORGANISM: Staphylococcus aureus
 US-10-172-425B-3

Query Match 66.7%; Score 22; DB 6; Length 10;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 Db 1 KKKVTAQELD 10

RESULT 15

US-10-172-425B-4
 ; Sequence 4, Application US/10172425B
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Arad, Gila
 ; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
 ; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
 ; CURRENT FILING DATE: 2002-06-13
 ; PRIOR APPLICATION NUMBER: US/10/172,425B
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: PCT/IL97/00438
 ; PRIOR FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: ISRAEL 119938
 ; PRIOR FILING DATE: 1996-12-30
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-10-172-425B-4

Query Match 66.7%; Score 22; DB 6; Length 10;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXXXTXQEXD 12
 Db 1 KKKATVQELD 10

Search completed: June 5, 2003, 15:52:27
 Job time : 34.1818 secs

OY 3 KXXXXXXXXLD 12
DB 73 KKTAAAFALD 82

RESULT 2

US-09-733-089-16924
Sequence 16924, Application US/09733089
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovacic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/733,089
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/474,435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 16924
LENGTH: 358
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-733-089-16924

Query Match 67.9%; Score 19; DB 21; Length 358;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXLD 12
DB 42 KKAADAAALD 51

RESULT 3

US-09-816-660-16924
Sequence 16924, Application US/09816660
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovacic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/816,660
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/474,435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/733,089
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER:) US 09/684,016
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 16924
LENGTH: 358
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-816-660-16924

Query Match 67.9%; Score 19; DB 22; Length 358;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXLD 12
DB 42 KKAADAAALD 51

RESULT 4

US-09-513-996A-43459
Sequence 43459, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 43459
LENGTH: 378
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: UNSURE
LOCATION: 1..378
OTHER INFORMATION: any n or xaa - unknown
FEATURE:
OTHER INFORMATION: Location 1..378 / Ceres Seq. ID 1985639
US-09-513-996A-43459

Query Match 67.9%; Score 19; DB 19; Length 378;
Best Local Similarity 40.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXLD 12
DB 13 KKAADAAALD 22

RESULT 5

US-09-708-427-18784
Sequence 18784, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18784
LENGTH: 378
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..378
OTHER INFORMATION: xaa is any amino acid.
NAME/KEY: misc-feature
LOCATION: 1..378
OTHER INFORMATION: Ceres Seq. ID 1834815
US-09-708-427-18784

Query Match 67.9%; Score 19; DB 21; Length 378;
Best Local Similarity 40.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXLD 12
DB 11

Db 13 KKAADAAALD 22

RESULT 6

US-09-791-537-114720
; Sequence 114720, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonoximix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 114720
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-791-537-114720

Query Match
Best Local Similarity 67.98; Score 19; DB 21; Length 378;
40.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 13 KKAADAAALD 22

RESULT 7

US-60-356-051-2815
; Sequence 2815, Application US/60356051
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Lufflyya, Linda L.
; TITLE OF INVENTION: NUCLEIC ACIDS AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
; FILE REFERENCE: 38-21 (15300)1
; CURRENT APPLICATION NUMBER: US/60/356,051
; CURRENT FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2815
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-60-356-051-2815

Query Match
Best Local Similarity 67.98; Score 19; DB 27; Length 378;
40.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 13 KKAADAAALD 22

RESULT 8

US-10-221-279-10068
; Sequence 10068, Application US/10221279
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-046
; CURRENT APPLICATION NUMBER: US/10/221,279
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07

; NUMBER OF SEQ ID NOS: 12360
; SOFTWARE: Custom
; SEQ ID NO 10068
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-279-10068

Query Match
Best Local Similarity 64.38; Score 18; DB 26; Length 35;
40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 3 KKYSSQTSLD 12

RESULT 9

PCT-US99-22853B-42
; Sequence 42, Application PC/TUS9922853B
; GENERAL INFORMATION:
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-0569F(PC)
; CURRENT APPLICATION NUMBER: PCT/US99/22853B
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 3938
; SOFTWARE: MS Word 97
; SEQ ID NO 42
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: LOCATION 1..43, Ceres Seq. ID 1685642
; NAME/KEY: UNSURE
; LOCATION: (1)..(43)
; OTHER INFORMATION: any Xaa - any amino acid, unknown or other
PCT-US99-22853B-42

Query Match
Best Local Similarity 64.38; Score 18; DB 1; Length 43;
40.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 5 KKLTTDALD 14

RESULT 10

PCT-US00-07527-111
; Sequence 111, Application PC/TUS0007527
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 47 Human Secreted Proteins
; FILE REFERENCE: PS529PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07527
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/126,600
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/171,550
; EARLIER FILING DATE: 1999-171,550
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 111
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07527-111

Query Match
Best Local Similarity 64.38; Score 18; DB 1; Length 46;
40.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 19 KKSAAESMLD 28

RESULT 11

PCT-US00-07527-112
; Sequence 112, Application PC/TUS0007527
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 47 Human Secreted Proteins
; FILE REFERENCE: P5529PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07527
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/126,600
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/171,550
; EARLIER FILING DATE: 1999-171,550
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07527-112

Query Match 64.3%; Score 18; DB 1; Length 46;
Best Local Similarity 40.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 19 KKSAAESMLD 28

RESULT 12

PCT-US99-22853B-41
; Sequence 41, Application PC/TUS9922853B
; GENERAL INFORMATION:
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-0569F(PC)
; CURRENT APPLICATION NUMBER: PCT/US99/22853B
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 3938
; SOFTWARE: MS Word 97
; SEQ ID NO 41
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: LOCATION 1..54, Ceres Seq. ID 1685641
; LOCATION: (1)..(54)
; OTHER INFORMATION: any xaa - any amino acid, unknown or other
PCT-US99-22853B-41

Query Match 64.3%; Score 18; DB 1; Length 54;
Best Local Similarity 40.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 16 KKLTTTDL 25

RESULT 13
PCT-US99-22853B-40
; Sequence 40, Application PC/TUS9922853B
; GENERAL INFORMATION:
; APPLICANT: Ceres, Inc.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-0569F(PC)
; CURRENT APPLICATION NUMBER: PCT/US99/22853B
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 3938
; SOFTWARE: MS Word 97
; SEQ ID NO 40
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: LOCATION 1..79, Ceres Seq. ID 1685640
; NAME/KEY: UNSURE
; LOCATION: (1)..(79)
; OTHER INFORMATION: any xaa - any amino acid, unknown or other
PCT-US99-22853B-40

Query Match 64.3%; Score 18; DB 1; Length 79;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 41 KKLTTTDL 50

RESULT 14

US-09-134-000-5378
; Sequence 5378, Application US/09134000A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
; FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134,000A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 5378
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000-5378

Query Match 64.3%; Score 18; DB 15; Length 87;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KXXXXXXXXD 12
DB 44 KKSRAFSMLD 53

RESULT 15

US-09-758-472-8508
; Sequence 8508, Application US/09758472
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PH001
; CURRENT APPLICATION NUMBER: US/09/758,472
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9632
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8508
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:


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; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-472-8508

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Query Match      64.3%; Score 18; DB 21; Length 89;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY      3 KKKXXXXLD 12
        ||      ||
Db      43 KKAIIAALD 52

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Search completed: June 5, 2003, 15:47:37
 Job time : 147.818 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:31:47 ; Search time 34,1818 Seconds
(without alignments)
74.544 Million cell updates/sec

Title: US-09-150-947f-17
Perfect score: 28
Sequence: 1 XXXXXXXXXXXXLD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1012620 segs, 21337834 residues

Total number of hits satisfying chosen parameters: 1012620

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
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2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
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6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	67.9	310	US-10-369-493-12686	Sequence 12686, A
2	19	67.9	378	US-10-361-942-986	Sequence 986, App
3	18	64.3	87	US-09-134-000C-5378	Sequence 5378, Ap
4	18	64.3	87	US-09-134-000C-5378	Sequence 5378, Ap
5	18	64.3	100	US-10-421-684-1170	Sequence 1170, Ap
6	18	64.3	109	US-09-724-676-55061	Sequence 55061, A
7	18	64.3	109	US-09-724-676-55061	Sequence 55061, A
8	18	64.3	147	US-09-513-999C-6288	Sequence 6288, Ap
9	18	64.3	147	US-09-513-999C-6288	Sequence 6288, Ap
10	18	64.3	152	US-09-949-016-6460	Sequence 6460, Ap
11	18	64.3	152	US-09-949-016-6460	Sequence 6460, Ap
12	18	64.3	161	US-09-724-676-55060	Sequence 55060, A
13	18	64.3	161	US-09-724-676-55060	Sequence 55060, A
14	18	64.3	252	US-10-282-122A-55371	Sequence 55371, A
15	18	64.3	252	US-10-282-122A-55371	Sequence 55371, A
16	18	64.3	315	US-10-431-652-4290	Sequence 4290, Ap
17	18	64.3	318	US-10-372-490-90	Sequence 90, App
18	18	64.3	318	US-10-372-490-90	Sequence 92, App
19	18	64.3	328	US-10-363-616-281	Sequence 281, App
20	18	64.3	341	US-10-272-490-68	Sequence 68, App
21	18	64.3	341	US-10-272-490-68	Sequence 68, App
22	18	64.3	341	US-10-214-473-68	Sequence 68, App
23	18	64.3	341	US-10-214-473-68	Sequence 68, App
24	18	64.3	406	US-10-425-114-70484	Sequence 70484, A
25	18	64.3	768	US-10-218-140-4424	Sequence 4424, Ap
26	18	64.3	837	US-10-369-493-12296	Sequence 22296, A

27	17	60.7	12	US-10-172-425B-53	Sequence 53, App
28	17	60.7	14	US-10-172-425B-37	Sequence 37, App
29	17	60.7	14	US-10-172-425B-49	Sequence 49, App
30	17	60.7	53	US-10-424-599-172320	Sequence 172320, App
31	17	60.7	57	US-10-424-599-172320	Sequence 172320, App
32	17	60.7	70	US-10-424-599-23335	Sequence 23335, App
33	17	60.7	77	US-10-424-599-23335	Sequence 23335, App
34	17	60.7	85	US-10-424-599-194596	Sequence 194596, App
35	17	60.7	106	US-09-864-408A-3042	Sequence 3042, App
36	17	60.7	109	US-10-424-599-167306	Sequence 167306, App
37	17	60.7	128	US-10-357-886-44	Sequence 44, App
38	17	60.7	142	US-09-857-826B-18	Sequence 18, App
39	17	60.7	143	US-10-276-774-2588	Sequence 2588, App
40	17	60.7	152	US-10-417-884-3744	Sequence 3744, App
41	17	60.7	160	US-10-424-599-170060	Sequence 170060, App
42	17	60.7	170	US-10-264-237-2676	Sequence 2676, App
43	17	60.7	178	US-10-282-122A-44631	Sequence 44631, A
44	17	60.7	189	US-10-094-749-2347	Sequence 2347, App
45	17	60.7	192	US-09-675-784A-8051	Sequence 8051, App

ALIGNMENTS

RESULT 1
US-10-369-493-12686
Sequence 12686, Application US/10369493
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12686
LENGTH: 310
TYPE: PRT
ORGANISM: Aspergillus nidulans
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(310)
OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-12686
Query Match 67.9%; Score 19; DB 6; Length 310;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 73 KKTAAAFALD 82
QY 3 KXXXXXXLD 12
||
||
||
RESULT 2
US-10-361-942-986
Sequence 986, Application US/10361942
GENERAL INFORMATION:
APPLICANT: Lutiya, Linda L.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(13300)K
CURRENT APPLICATION NUMBER: US/10/361,942
PRIOR FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/356,051
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 2906

SEQ ID NO 986
LENGTH: 378
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: Clone ID: AT_T6A23.C1.p24.tg
US-10-361-942-986

Query Match 67.9%; Score 19; DB 6; Length 378;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
DB 13 KKAADAAALD 22

RESULT 3
US-09-134-000C-5378
Sequence 5378, Application US/09134000C

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5378
LENGTH: 87
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5378

Query Match 64.3%; Score 18; DB 5; Length 87;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
DB 44 KKSRAFASLD 53

RESULT 4
US-09-134-000C-5378
Sequence 5378, Application US/09134000C

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5378
LENGTH: 87
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5378

Query Match 64.3%; Score 18; DB 5; Length 87;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
DB 44 KKSRAFASLD 53

RESULT 5
US-10-421-684-1170
Sequence 1170, Application US/10421684

GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mitanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/10/421,684
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US/09/732,210
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1170
LENGTH: 100
TYPE: PRT
ORGANISM: Marchantia polymorpha
US-10-421-684-1170

Query Match 64.3%; Score 18; DB 6; Length 100;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
DB 29 KKITETSSLD 38

RESULT 6
US-09-724-676-55061
Sequence 55061, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55061
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-55061

Query Match 64.3%; Score 18; DB 5; Length 109;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 KKKXXXXXLD 12
DB 44 KKSAAESMLD 53

RESULT 7
US-09-724-676A-55061
Sequence 55061, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2
SEQ ID NO 55061
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-55061

Query Match
Best Local Similarity 64.3%; Score 18; DB 5; Length 109;
40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXID 12
DB 44 KKSAAESMID 53

RESULT 8
US-09-513-999C-6288
Sequence 6288, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Maline Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, 052, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6288
LENGTH: 147
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6288

Query Match
Best Local Similarity 64.3%; Score 18; DB 5; Length 147;
40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXID 12
DB 78 KKKRAATID 87

RESULT 9
US-09-513-999C-6288
Sequence 6288, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Maline Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, 052, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6288
LENGTH: 147
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6288

Query Match
Best Local Similarity 64.3%; Score 18; DB 5; Length 147;
40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXID 12
DB 78 KKKRAATID 87

DB 78 KKKRAATID 87

RESULT 10
US-09-949-016-6460
Sequence 6460, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6460
LENGTH: 152
TYPE: PRT
ORGANISM: Human
US-09-949-016-6460

Query Match
Best Local Similarity 64.3%; Score 18; DB 5; Length 152;
40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXID 12
DB 44 KKSAAESMID 53

RESULT 11
US-60-440-068-114
Sequence 114, Application US/60440068
GENERAL INFORMATION:
APPLICANT: MADLER, STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 114
LENGTH: 152
TYPE: PRT
ORGANISM: Homo sapiens
US-60-440-068-114

Query Match
Best Local Similarity 64.3%; Score 18; DB 7; Length 152;
40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXID 12
DB 44 KKSAAESMID 53

RESULT 12
US-09-724-676-55060
Sequence 55060, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181, 4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55060
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-55060

Query Match 64.3%; Score 18; DB 5; Length 161;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 44 KKSAAESMLD 53

RESULT 13
US-09-724-676A-55060
Sequence 55060, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55060
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-55060

Query Match 64.3%; Score 18; DB 5; Length 161;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 44 KKSAAESMLD 53

RESULT 14
US-10-282-122A-52371
Sequence 52371, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trivick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52371
LENGTH: 252
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52371

Query Match 64.3%; Score 18; DB 6; Length 252;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 9 KKASTDFTMD 18

RESULT 15
US-10-431-652-7651
Sequence 7651, Application US/10431652
GENERAL INFORMATION:
APPLICANT: Breton, Gary L.
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
FILE REFERENCE: PATH03-08
CURRENT APPLICATION NUMBER: US/10/431,652
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 09/328,352
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 60/088,701
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7651
LENGTH: 254
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-10-431-652-7651

Query Match 64.3%; Score 18; DB 6; Length 254;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 KKKXXXXXLD 12
||
Db 210 KKSOGSKTMD 219

Search completed: June 5, 2003, 15:52:27
JOB time : 34.1818 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 15:29:17 ; Search time 147.818 Seconds

(without alignments)
52.340 Million cell updates/sec

Title: US-09-150-947F-18

Perfect score: 17
Sequence: 1 xxxxxxxxxxxx 12Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.3	2	1	PCT-US00-00358-13	Sequence 13, Appl
2	35.3	2	1	PCT-US00-08879-16	Sequence 16, Appl
3	35.3	2	1	PCT-US00-08879-18	Sequence 18, Appl
4	35.3	2	1	PCT-US00-08879-30	Sequence 30, Appl
5	35.3	2	1	PCT-US00-08879A-16	Sequence 16, Appl
6	35.3	2	1	PCT-US00-08879A-18	Sequence 18, Appl

7	35.3	2	1	PCT-US00-08879A-30	Sequence 30, Appl
8	35.3	2	1	PCT-US02-09188-532	Sequence 532, App
9	35.3	2	1	PCT-US02-09339-152	Sequence 152, App
10	35.3	2	1	PCT-US02-09370-551	Sequence 551, App
11	35.3	2	1	PCT-US02-23763-296	Sequence 296, App
12	35.3	2	1	PCT-US02-30452-85	Sequence 85, App
13	35.3	2	3	PCT-US99-26100-6	Sequence 6, Appl1
14	35.3	2	3	US-07-853-042A-3	Sequence 3, Appl1
15	35.3	2	6	US-08-222-6236A-122	Sequence 122, App
16	35.3	2	6	US-08-248-816-8	Sequence 8, Appl1
17	35.3	2	8	US-08-430-121-8	Sequence 8, Appl1
18	35.3	2	8	US-08-472-679B-15	Sequence 15, Appl
19	35.3	2	8	US-08-472-679B-23	Sequence 23, Appl
20	35.3	2	8	US-08-472-679B-33	Sequence 33, Appl
21	35.3	2	8	US-08-472-679B-39	Sequence 39, Appl
22	35.3	2	8	US-08-472-679D-15	Sequence 15, Appl
23	35.3	2	8	US-08-472-679D-23	Sequence 23, Appl
24	35.3	2	8	US-08-472-679D-33	Sequence 33, Appl
25	35.3	2	8	US-08-472-679D-39	Sequence 39, Appl
26	35.3	2	8	US-08-472-679H-15	Sequence 15, Appl
27	35.3	2	8	US-08-472-679H-23	Sequence 23, Appl
28	35.3	2	8	US-08-472-679H-33	Sequence 33, Appl
29	35.3	2	8	US-08-472-679H-39	Sequence 39, Appl
30	35.3	2	10	US-08-633-879B-85	Sequence 85, Appl
31	35.3	2	11	US-08-783-79B-85	Sequence 85, Appl
32	35.3	2	12	US-08-843-675A-72	Sequence 72, Appl
33	35.3	2	16	US-09-295-846A-24	Sequence 24, Appl
34	35.3	2	16	US-09-295-846A-26	Sequence 26, Appl
35	35.3	2	16	US-09-295-846A-38	Sequence 38, Appl
36	35.3	2	16	US-09-295-846A-46	Sequence 46, Appl
37	35.3	2	16	US-09-295-846A-52	Sequence 52, Appl
38	35.3	2	16	US-09-295-846A-58	Sequence 58, Appl
39	35.3	2	16	US-09-295-846A-64	Sequence 64, Appl
40	35.3	2	16	US-09-295-846A-70	Sequence 70, Appl
41	35.3	2	16	US-09-295-846A-76	Sequence 76, Appl
42	35.3	2	16	US-09-295-846A-82	Sequence 82, Appl
43	35.3	2	16	US-09-295-846A-88	Sequence 88, Appl
44	35.3	2	16	US-09-295-846A-94	Sequence 94, Appl
45	35.3	2	16	US-09-295-846A-100	Sequence 100, Appl

ALIGNMENTS

RESULT 1
PCT-US00-00358-13
Sequence 13, Application PC/TUS0000358
GENERAL INFORMATION:
APPLICANT: pecker, iris
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY DISTANTLY HOM
FILE REFERENCE: 00/20105
CURRENT APPLICATION NUMBER: PCT/US00/00358
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/140,801
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-00358-13

Query Match 35.3%, Score 6, DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.4e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 D 12
Db 1 D 1

RESULT 2
PCT-US00-08879-16
; Sequence 16, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-16

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
|
Db 1 D 1

RESULT 3
PCT-US00-08879-18
; Sequence 18, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-18

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
|
Db 1 D 1

RESULT 4
PCT-US00-08879-30
; Sequence 30, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT

; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-30

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
|
Db 2 D 2

RESULT 5
PCT-US00-08879A-16
; Sequence 16, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-16

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
|
Db 1 D 1

RESULT 6
PCT-US00-08879A-18
; Sequence 18, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-18

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 7

PCT-US00-08879A-30
; Sequence 30, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-30

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 2 D 2

RESULT 8

PCT-US02-09188-532
; Sequence 532, Application PC/TUS0209188
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS952PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09188
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1732
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 532
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09188-532

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 9

PCT-US02-09239-152
; Sequence 152, Application PC/TUS0209239
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS953PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09239
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 152
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09239-152

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 10

PCT-US02-09370-551
; Sequence 551, Application PC/TUS0209370
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS954PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09370
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1834
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 551
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09370-551

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 11

PCT-US02-23763-296
; Sequence 296, Application PC/TUS0223763
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MHB 01-1017
; CURRENT APPLICATION NUMBER: PCT/US02/23763
; CURRENT FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: US 60/308,523
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/351,289
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/366,854
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 60/385,362
PRIOR FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 307
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 296
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-23763-296

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 12
PCT-US02-30452-85
Sequence 85, Application PC/TUS0230452
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
FILE REFERENCE: 08702.00012-00304
CURRENT APPLICATION NUMBER: PCT/US02/30452
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: 60/324,528
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 85
LENGTH: 2
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-30452-85

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 13
PCT-US99-26100-6
Sequence 6, Application PC/TUS9926100
GENERAL INFORMATION:
APPLICANT: Ream, Walt et al.
TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
FILE REFERENCE: 53629
CURRENT APPLICATION NUMBER: PCT/US99/26100
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: 60/107,185
EARLIER FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 6
LENGTH: 2
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
PCT-US99-26100-6

Query Match 35.3%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 2 D 2

RESULT 14
US-07-853-042A-3
Sequence 3, Application US/07853042A
GENERAL INFORMATION:
APPLICANT: Anders BIL
TITLE OF INVENTION: METHOD AND MEANS FOR INDUCING, RESP.,
TITLE OF INVENTION: PREVENTING CONSTRUCTION OF THE PUPIL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FRED PHILPITT
STREET: 99 Canal Center Plaza, Ste. 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,042A
FILING DATE: 19920318
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FRED PHILPITT
REGISTRATION NUMBER: 16825
REFERENCE/DOCKET NUMBER: PHE-808
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
US-07-853-042A-3

Query Match 35.3%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 15
US-08-222-626A-122
Sequence 122, Application US/08222626A
GENERAL INFORMATION:
APPLICANT: Aral, Naoko
APPLICANT: Masuda, Esteban S.
APPLICANT: Tokumitsu, Hiroshi
TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California

COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/222,626A
 FILING DATE: 04-APR-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/148,061
 FILING DATE: 05-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/113,971
 FILING DATE: 30-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/088,998
 FILING DATE: 30-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/088,483
 FILING DATE: 06-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0392K3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 122:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-222-626A-122

Query Match 35.3%; Score 6; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 D 12
 Db 1 D 1

Search completed: June 5, 2003, 15:47:38
 Job time: 148.818 secs

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OM protein - protein search, using SW model

Run on: June 5, 2003, 15:31:47 ; Search time 34.1818 Seconds
(Without alignments)
74.544 Million cell updates/sec

Title: US-09-150-947F-18

Perfect score: 17
Sequence: 1 XXXXXXXXXXXXD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1012620 seqs, 212337834 residues

Total number of hits satisfying chosen parameters: 1012620

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	35.3	2	4	US-08-472-679H-15
2	6	35.3	2	4	US-08-472-679H-23
3	6	35.3	2	4	US-08-472-679H-33
4	6	35.3	2	4	US-08-472-679H-39
5	6	35.3	2	4	US-08-472-679H-15
6	6	35.3	2	4	US-08-472-679H-23
7	6	35.3	2	4	US-08-472-679H-33
8	6	35.3	2	4	US-08-472-679H-39
9	6	35.3	2	6	US-10-187-339-6
10	6	35.3	2	6	US-10-109-048-461
11	6	35.3	2	6	US-10-405-027-5115
12	6	35.3	3	1	PCT-US02-14358-15
13	6	35.3	3	1	PCT-US02-14358-16
14	6	35.3	3	1	PCT-US02-14358-17
15	6	35.3	3	1	PCT-US02-14358-18
16	6	35.3	3	1	PCT-US02-14358-19
17	6	35.3	3	1	PCT-US02-14358-20
18	6	35.3	3	1	PCT-US02-21322-6
19	6	35.3	3	1	PCT-US02-21322A-6
20	6	35.3	3	1	PCT-US02-26918A-316
21	6	35.3	3	1	PCT-US02-26918A-317
22	6	35.3	3	1	PCT-US02-26918A-318
23	6	35.3	3	1	PCT-US02-26918A-319
24	6	35.3	3	1	PCT-US03-00079-30
25	6	35.3	3	1	PCT-US03-10473-6
26	6	35.3	3	1	PCT-US03-11798-8

27	6	35.3	3	1	PCT-US03-14096-24	Sequence 24, App1
28	6	35.3	3	5	US-09-302-195C-1	Sequence 1, App1
29	6	35.3	3	5	US-09-716-394-11	Sequence 11, App1
30	6	35.3	3	5	US-09-853-080A-37	Sequence 37, App1
31	6	35.3	3	5	US-09-772-819-11	Sequence 11, App1
32	6	35.3	3	5	US-09-573-830-11	Sequence 11, App1
33	6	35.3	3	5	US-09-992-124B-74	Sequence 74, App1
34	6	35.3	3	5	US-09-564-045-11	Sequence 11, App1
35	6	35.3	3	5	US-09-867-847A-30	Sequence 30, App1
36	6	35.3	3	5	US-09-980-347-6	Sequence 6, App1
37	6	35.3	3	5	US-09-723-437B-11	Sequence 11, App1
38	6	35.3	3	5	US-09-939-481-81	Sequence 81, App1
39	6	35.3	3	5	US-09-898-165B-33	Sequence 33, App1
40	6	35.3	3	5	US-09-623-548A-1053	Sequence 1053, App1
41	6	35.3	3	5	US-09-623-548A-1054	Sequence 1054, App1
42	6	35.3	3	5	US-09-623-548A-1160	Sequence 1160, App1
43	6	35.3	3	5	US-09-623-548A-1170	Sequence 1170, App1
44	6	35.3	3	6	US-10-141-531-15	Sequence 15, App1
45	6	35.3	3	6	US-10-141-531-16	Sequence 16, App1

ALIGNMENTS

RESULT 1

US-08-472-679H-15
Sequence 15, Application US/08472679H

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.
Junker, David E.

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 267

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pamela G. Salkeld

STREET: 2000 Galloping Hill Road

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,679H

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Salkeld, Pamela G.

REGISTRATION NUMBER: 38,607

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 298-2135

TELEFAX: (908) 298-5388

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-472-679H-15

Query Match

Best Local Similarity 100.0%; Pred. No. 7.6e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12

Db 1 D 1

RESULT 2

US-08-472-679H-23
; Sequence 23, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-472-679H-23
Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 D 12
DB 1 D 1
RESULT 3
US-08-472-679H-33
; Sequence 33, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33
Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 D 12
DB 1 D 1
RESULT 5
US-08-472-679H-15
; Sequence 15, Application US/08472679H

REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33

Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 D 12
DB 1 D 1

RESULT 4
US-08-472-679H-39
; Sequence 39, Application US/08472679H
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,679H
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Salkeld, Pamela G.
; REGISTRATION NUMBER: 38,607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2135
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-08-472-679H-39

Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 D 12
DB 1 D 1

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-472-679H-15

Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 6
US-08-472-679H-23
Sequence 23, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-472-679H-15

TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-472-679H-23

Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 7
US-08-472-679H-33
Sequence 33, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-472-679H-33

Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 D 12
DB 1 D 1

RESULT 8
US-08-472-679H-39
Sequence 39, Application US/08472679H
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.

Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pamela G. Salkeld
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-08-472-679H-39

Query Match 35.3%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 9
US-10-187-339-6
; Sequence 6, Application US/10187339
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; FILE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/10/187,339
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/434,837
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,185
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-187-339-6

Query Match 35.3%; Score 6; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 2 D 2

RESULT 10
US-10-109-048-461
; Sequence 461, Application US/10109048
; GENERAL INFORMATION:
; APPLICANT: COMODI, PADMA
; APPLICANT: KEELING, PETER L.
; APPLICANT: RAMIREZ, NONA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO, ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109,048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279,720
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 461
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Accession No. 3832512
US-10-109-048-461

Query Match 35.3%; Score 6; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 2 D 2

RESULT 11
US-10-405-027-5115
; Sequence 5115, Application US/10405027
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS806P1
; CURRENT APPLICATION NUMBER: US/10/405,027
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/369,608
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/376,175
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 5810
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5115
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-405-027-5115

Query Match 35.3%; Score 6; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
DB 1 D 1

RESULT 12
PCT-US02-14358-15
; Sequence 15, Application PC/TUS0214358
; GENERAL INFORMATION:
; APPLICANT: XENCOR
; APPLICANT: SYNGENTA PARTICIPATIONS AG
; APPLICANT: Briggs, Steven P.

APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Luginduhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RPT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 3
TYPE: PRT
ORGANISM: Escherichia coli
PCT-US02-14358-15

Query Match 35.3%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
|
Db 1 D 1

RESULT 13
PCT-US02-14358-16
Sequence 16, Application PC/TUS0214358
GENERAL INFORMATION:
APPLICANT: XENCOR
APPLICANT: SYNGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Luginduhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RPT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 3
TYPE: PRT
ORGANISM: Bacillus subtilis
PCT-US02-14358-16

Query Match 35.3%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 D 12
|
Db 1 D 1

RESULT 14
PCT-US02-14358-17
Sequence 17, Application PC/TUS0214358
GENERAL INFORMATION:

APPLICANT: XENCOR
APPLICANT: SYNGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Luginduhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: FP-71457-2-PC/RPT/RMS/RMK
CURRENT APPLICATION NUMBER: PCT/US02/14358
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 3
TYPE: PRT
ORGANISM: Mycobacterium leprae
PCT-US02-14358-17

Query Match 35.3%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 D 1

RESULT 15
PCT-US02-14358-18
Sequence 18, Application PC/TUS0214358
GENERAL INFORMATION:
APPLICANT: XENCOR
APPLICANT: SYNGENTA PARTICIPATIONS AG
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Helfetz, Peter
APPLICANT: Luginduhl, Peter
APPLICANT: Muchhal, Umesh
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NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 3
TYPE: PRT
ORGANISM: Sarccharomyces cerevisiae
PCT-US02-14358-18

Query Match 35.3%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 7.6e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 D 1

Search completed: June 5, 2003, 15:52:28

Fri Jun 6 09:14:59 2003

Job time : 35.1818 secs

us-09-150-947f-18.rapn

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